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168409

me

From: Mertz, Prema
Sent: Wednesday, October 12, 2005 1:30 PM
To: STIC-Biotech/ChemLib
Subject: 10/666,225

Please search any 6 amino acids of SEQ ID NO:14 with protein databases.

Please search US PG PUB databases with SEQ ID NO:14.

Thanks.

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Searcher: _____
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Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____
Searcher: Beverly e 2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC
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Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ _____ Other CGN

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2005, 18:35:50 ; Search time 42 Seconds
(without alignments)
801.806 Million cell updates/sec

Title: US-10-666-225-14
Perfect score: 350
Sequence: 1 MRLPDVQLMLVLLMALVRAQ.....NGNVKTDVDPDVVEACGCS 350

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1748

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	67	19.1	350	2	JC5241	activin beta E cha
2	15	4.3	352	2	JC2466	inhibin beta-C cha
3	11	3.1	352	2	S70580	activin beta C pre
4	11	3.1	352	2	JC5366	activin beta C - m
5	9	2.6	151	2	G43296	bone morphogenetic
6	8	2.3	283	2	T14455	hypothetical prote
7	8	2.3	311	2	D86425	unknown protein [l
8	8	2.3	367	2	JC4151	activin beta D cha
9	8	2.3	480	2	S22701	mannosyltransferas
10	8	2.3	1045	2	A29840	serine proteinase
11	8	2.3	1060	2	S63993	acrosomal protein
12	8	2.3	1273	2	E72611	probable ATP-depen
13	7	2.0	72	2	S28793	major merozoite su
14	7	2.0	86	2	G84229	hypothetical prote
15	7	2.0	129	2	AH3212	hypothetical prote
16	7	2.0	130	2	F72513	hypothetical prote
17	7	2.0	135	2	H82641	hypothetical prote
18	7	2.0	169	2	C95394	hypothetical prote
19	7	2.0	183	2	H63561	protein (imported
20	7	2.0	184	2	B87708	hypothetical prote
21	7	2.0	189	2	B69005	hypothetical prote
22	7	2.0	198	2	S48236	probable 2-oxogluc
23	7	2.0	233	2	A25814	SMI protein - yea
24	7	2.0	237	2	A64013	glycoprotein 185 -
25	7	2.0	237	2	D40595	hypothetical prote
26	7	2.0	243	2	B96010	hypothetical prote
27	7	2.0	244	2	AF2753	conserved hypothet
28	7	2.0	245	2	S34242	transcription regu
29	7	2.0	247	2	G83798	hypothetical prote
						ABC transporter (A

30	7	2.0	252	2	D97534	probable transcrip
31	7	2.0	274	2	A71275	hypothetical prote
32	7	2.0	281	2	B54498	major merozoite su
33	7	2.0	283	2	T36640	probable ABC-type
34	7	2.0	291	2	AF1722	post-translocation
35	7	2.0	292	2	T09784	homeobox leucine z
36	7	2.0	303	2	H75528	conserved hypothet
37	7	2.0	315	2	T10805	annexin - upland c
38	7	2.0	316	2	T31428	fiber annexin - up
39	7	2.0	334	2	T46885	3-methyl-2-oxobuta
40	7	2.0	334	2	T36511	probable branched-
41	7	2.0	338	2	AD3103	hypothetical prote
42	7	2.0	356	2	S16907	collagen alpha 1(I
43	7	2.0	362	2	H75398	probable succinyl-
44	7	2.0	371	2	B83781	two-component sens
45	7	2.0	378	2	AC1942	hypothetical prote
46	7	2.0	382	2	D75398	hypothetical prote
47	7	2.0	394	2	F69401	cell division prot
48	7	2.0	397	2	C82992	hypothetical prote
49	7	2.0	421	1	I64185	cell division prot
50	7	2.0	442	2	E72029	thiophene/furan ox
51	7	2.0	442	2	D86595	thiophene/furan ox
52	7	2.0	445	2	T47813	hypothetical prote
53	7	2.0	452	2	G70905	hypothetical prote
54	7	2.0	467	2	F64765	hypothetical prote
55	7	2.0	471	2	AB3422	yeast protein - Bac
56	7	2.0	474	2	D83396	glutamyl-tRNA(gln)
57	7	2.0	495	2	B71311	conserved hypothet
58	7	2.0	500	2	C64043	probable thiophene
59	7	2.0	506	2	T29968	citrate (pro-3S)-1
60	7	2.0	546	2	D83408	hypothetical prote
61	7	2.0	581	2	C82043	hypothetical prote
62	7	2.0	588	2	TS1154	conserved hypothet
63	7	2.0	600	2	JC7725	probable transmemb
64	7	2.0	602	2	G83388	mycodextranase (EC
65	7	2.0	652	2	T34497	probable binding p
66	7	2.0	668	2	AH0806	hypothetical prote
67	7	2.0	668	2	T11778	phosphoglycerate t
68	7	2.0	723	2	S70098	phosphoglycerate t
69	7	2.0	753	2	G70184	probable membrane
70	7	2.0	763	2	A47563	methyl-accepting c
71	7	2.0	784	2	G95112	glucose-6-phosphat
72	7	2.0	784	2	F97981	exoribonuclease, R
73	7	2.0	804	2	T05783	hypothetical prote
74	7	2.0	848	2	B89042	protein P14P9.3 [l
75	7	2.0	872	2	T10582	hypothetical prote
76	7	2.0	889	1	S47162	DNA-directed RNA p
77	7	2.0	917	1	RDMUNH	nitrate reductase
78	7	2.0	941	2	C75633	ATP-dependent heli
79	7	2.0	962	1	SNECPI	pitriclysin (EC 3.4
80	7	2.0	962	2	H85933	proteinase III [im
81	7	2.0	962	2	F91088	proteinase III [im
82	7	2.0	968	2	T29532	hypothetical prote
83	7	2.0	974	2	T29007	translacion elonga
84	7	2.0	1029	2	T30852	outer membrane pro
85	7	2.0	1039	2	T35878	hypothetical prote
86	7	2.0	1049	1	CGB07S	collagen alpha 1(I
87	7	2.0	1049	2	A27079	fibronectin recept
88	7	2.0	1058	2	A38564	ubiquitin-protein
89	7	2.0	1058	2	JC1254	ubiquitin-protein
90	7	2.0	1060	2	S06286	major merozoite su
91	7	2.0	1086	2	S16752	major merozoite su
92	7	2.0	1231	2	C84716	hypothetical prote
93	7	2.0	1487	1	EDBEE1	immediate-early pr
94	7	2.0	1487	1	EDBEF6	155k transcription
95	7	2.0	1488	2	AG2136	polyketide synthas
96	7	2.0	1631	1	SAZOK1	major merozoite su
97	7	2.0	1639	2	S05603	major merozoite su
98	7	2.0	1640	2	A24594	probable major sur
99	7	2.0	1669	1	CGHU4B	collagen alpha 1(I
100	7	2.0	1669	1	CGMS4B	collagen alpha 1(I
101	7	2.0	1701	2	A26868	major merozoite su
102	7	2.0	1701	2	A54498	major merozoite su

103	7	2.0	1708	2	F69189	protoporphyrix IX
104	7	2.0	1726	1	SAZQM	major merozoite su
105	7	2.0	1726	2	A45948	major merozoite su
106	7	2.0	1894	2	C54689	protein-tyrosine-p
107	7	2.0	2021	2	A97859	190-KDa cell surfa
108	7	2.0	2249	2	A41477	190K surface antig
109	7	2.0	3169	2	T00296	toxin B - Escheric
110	7	2.0	3972	2	S75251	hypothetical prote
111	6	1.7	33	2	B26762	protamine (mugilin
112	6	1.7	34	1	TYTVY2	protamine Y2 - blu
113	6	1.7	57	2	E87352	hypothetical prote
114	6	1.7	61	2	S18336	hypothetical prote
115	6	1.7	67	2	A38226	CAMP-dependent pro
116	6	1.7	68	2	D72428	hypothetical prote
117	6	1.7	69	2	T17938	hypothetical prote
118	6	1.7	74	2	S77212	hypothetical prote
119	6	1.7	74	2	E69871	hypothetical prote
120	6	1.7	74	2	F97551	hypothetical prote
121	6	1.7	75	2	D84003	hypothetical prote
122	6	1.7	76	2	I45885	elastin - bovine (
123	6	1.7	76	2	B71840	hypothetical prote
124	6	1.7	76	2	B64675	conserved hypothet
125	6	1.7	80	2	G95414	hypothetical prote
126	6	1.7	86	2	AD0621	probable bacteriop
127	6	1.7	88	2	E87415	hypothetical prote
128	6	1.7	88	2	S77426	hypothetical prote
129	6	1.7	88	2	H83765	hypothetical prote
130	6	1.7	89	2	D72269	conserved hypothet
131	6	1.7	92	2	UC1136	major allergen cha
132	6	1.7	92	2	A56413	major allergen Fel
133	6	1.7	95	1	WTRBM1	macrophage antibio
134	6	1.7	95	1	S73274	defensin CS-4 prec
135	6	1.7	95	1	S55624	hypothetical prote
136	6	1.7	95	2	AG2795	hypothetical prote
137	6	1.7	96	2	G97574	conserved hypothet
138	6	1.7	96	2	T10870	hypothetical 11.0K
139	6	1.7	96	2	AC0034	y4kp protein - Rhl
140	6	1.7	97	2	T17020	probable type III
141	6	1.7	99	2	A12695	auxin-induced prot
142	6	1.7	99	2	E72533	hypothetical prote
143	6	1.7	101	2	PH1077	Ig light chain V r
144	6	1.7	102	2	C64308	hypothetical prote
145	6	1.7	103	2	UC5411	hypothetical prote
146	6	1.7	103	2	S75861	cortistatin-like p
147	6	1.7	105	2	S37489	ribosomal protein
148	6	1.7	105	2	AI2347	30S ribosomal prot
149	6	1.7	105	2	S70134	probable membrane
150	6	1.7	105	2	D69447	hypothetical prote
151	6	1.7	106	2	E72476	hypothetical prote
152	6	1.7	106	2	L7RB	Ig lambda chain C
153	6	1.7	109	1	T48748	probable glutaredo
154	6	1.7	109	2	AG0673	probable secreted
155	6	1.7	109	2	B28302	beta-galactoside-b
156	6	1.7	110	2	T12779	hypothetical prote
157	6	1.7	111	2	G98105	transcription regu
158	6	1.7	112	2	A46024	neurofilament-L su
159	6	1.7	113	2	S26278	T cell receptor be
160	6	1.7	114	2	S17380	T-cell receptor be
161	6	1.7	114	2	S48982	hypothetical prote
162	6	1.7	114	2	PN0504	activin beta A cha
163	6	1.7	115	2	D33932	Ig mu chain precur
164	6	1.7	115	2	D75507	hypothetical prote
165	6	1.7	115	2	HVMS31	Ig heavy chain pre
166	6	1.7	116	1	RGECD	modulator protein
167	6	1.7	116	1	A75111	hypothetical prote
168	6	1.7	117	1	HVCOE1	Ig heavy chain pre
169	6	1.7	117	1	B30505	Ig lambda-6 chain
170	6	1.7	118	2	A30505	Ig lambda chain C
171	6	1.7	118	2	T35585	hypothetical prote
172	6	1.7	118	2	E70161	ribosomal protein
173	6	1.7	119	2	S45992	probable membrane
174	6	1.7	119	2		
175	6	1.7	119	2		
176	6	1.7	120	2	S30770	ribosomal protein
177	6	1.7	120	2	B97067	uncharacterized pr
178	6	1.7	120	2	G97833	hypothetical prote
179	6	1.7	121	2	S64508	hypothetical prote
180	6	1.7	122	2	F72636	hypothetical prote
181	6	1.7	123	2	S63055	probable membrane
182	6	1.7	124	2	C83137	hypothetical prote
183	6	1.7	125	2	E83746	PTS system, glucit
184	6	1.7	125	2	S43295	bone morphogenetic
185	6	1.7	129	2	S05342	DNA-directed RNA p
186	6	1.7	129	2	AH2003	hypothetical prote
187	6	1.7	129	2	G70667	hypothetical prote
188	6	1.7	133	2	AB3465	hypothetical prote
189	6	1.7	134	2	B87022	probable membrane
190	6	1.7	135	1	LNHUGB	galactin 1 [valida
191	6	1.7	136	2	S07637	Ig heavy chain V r
192	6	1.7	136	2	D64324	ribosomal protein
193	6	1.7	137	1	AVMS35	Ig heavy chain pre
194	6	1.7	138	2	T45371	ribosomal protein
195	6	1.7	138	2	G70642	probable ribosomal
196	6	1.7	138	2	H87362	organic hydroperox
197	6	1.7	139	2	AF0685	hypothetical prote
198	6	1.7	139	2	PC4217	hypothetical 139 p
199	6	1.7	139	2	D95896	conserved hypothet
200	6	1.7	140	2	S14179	hypothetical prote
201	6	1.7	140	2	S04165	hypothetical prote
202	6	1.7	140	2	C69080	conserved hypothet
203	6	1.7	140	2	T10589	hypothetical prote
204	6	1.7	140	2	T36136	hypothetical prote
205	6	1.7	141	2	AB0110	conserved hypothet
206	6	1.7	141	2	E95241	transcription regu
207	6	1.7	142	2	B72683	hypothetical prote
208	6	1.7	142	2	B87653	CheB protein [lipo
209	6	1.7	143	1	GDBY	glutaredoxin - yea
210	6	1.7	145	2	S32213	hypothetical prote
211	6	1.7	145	2	AI2869	NTP pyrophosphohyd
212	6	1.7	145	2	AI3048	transcription regu
213	6	1.7	145	2	B98237	probable regulator
214	6	1.7	146	2	T36476	hypothetical prote
215	6	1.7	146	2	H75394	conserved hypothet
216	6	1.7	147	2	D71540	hypothetical prote
217	6	1.7	147	2	C97646	hypothetical prote
218	6	1.7	150	2	I59431	PR310 C-K-ras onco
219	6	1.7	150	2	T34697	probable insertion
220	6	1.7	151	2	E83550	positive regulator
221	6	1.7	151	2	AE1929	hypothetical prote
222	6	1.7	152	2	A71682	hypothetical prote
223	6	1.7	153	2	T47392	hypothetical prote
224	6	1.7	153	2	F71902	hypothetical prote
225	6	1.7	153	2	T52498	xanthine-guanine p
226	6	1.7	153	2	S28699	hypothetical prote
227	6	1.7	155	2	F87696	hypothetical prote
228	6	1.7	155	2	B85814	DNA mismatch endon
229	6	1.7	156	2	B90966	DNA mismatch endon
230	6	1.7	156	2	JS0264	DNA mismatch endon
231	6	1.7	157	2	S36538	B6 protein - human
232	6	1.7	157	2	D82209	probable antioxidant
233	6	1.7	157	2	B69221	conserved hypothet
234	6	1.7	158	2	AI2382	hypothetical prote
235	6	1.7	159	2	S57630	hypothetical prote
236	6	1.7	160	2	T37000	probable transposa
237	6	1.7	160	2	A35261	Alginatase regulator
238	6	1.7	161	1	HMECA1	hemagglutinin AFA-
239	6	1.7	161	2	T04981	hypothetical prote
240	6	1.7	163	2	A70847	hypothetical prote
241	6	1.7	164	2	AE3299	phosphinothricin N
242	6	1.7	164	2	T37174	protein-tyrosine-p
243	6	1.7	164	2	F72470	hypothetical prote
244	6	1.7	165	2	T36981	probable insertion
245	6	1.7	167	2	A82046	probable periplasm
246	6	1.7	169	1	S18946	ultra high-sulfur
247	6	1.7	169	2	S76048	hypothetical prote
248	6	1.7	169	2	G70627	hypothetical prote

395	6	1.7	250	2	C64546	conserved hypothet
396	6	1.7	250	2	AE3261	hypothetical prote
397	6	1.7	250	2	D75343	conserved hypothet
398	6	1.7	252	2	I50126	MHC class II histo
399	6	1.7	252	2	G97851	hypothetical prote
400	6	1.7	253	2	D71975	hypothetical prote
401	6	1.7	253	2	E64532	hypothetical prote
402	6	1.7	253	2	A84278	hypothetical prote
403	6	1.7	253	2	AI2872	hypothetical prote
404	6	1.7	254	2	AF0521	pyruvate dehydroge
405	6	1.7	254	2	A97311	uncharacterized pr
406	6	1.7	255	2	T38115	probable ATP-depen
407	6	1.7	256	2	T50892	spheroidene monoox
408	6	1.7	257	2	T10586	small nuclear ribo
409	6	1.7	257	2	I40170	hypothetical prote
410	6	1.7	258	2	I46080	uroglakin Ia - bov
411	6	1.7	259	2	E81146	conserved hypothet
412	6	1.7	259	2	D95298	probable 4-carboxy
413	6	1.7	261	2	H86636	chromosome partiti
414	6	1.7	261	2	C84776	hypothetical prote
415	6	1.7	262	2	AI0053	probable metalloen
416	6	1.7	262	2	AB1071	ferric iron reduct
417	6	1.7	262	2	S56594	ferrichrome-iron r
418	6	1.7	262	2	G91294	ferric iron reduct
419	6	1.7	262	2	B86136	ferric iron reduct
420	6	1.7	262	2	H70953	hypothetical prote
421	6	1.7	263	2	T03162	tegument protein 6
422	6	1.7	263	2	T17302	hypothetical prote
423	6	1.7	265	2	T44414	hypothetical prote
424	6	1.7	265	2	H84422	probable ribose 5-
425	6	1.7	265	2	E87357	hypothetical prote
426	6	1.7	265	2	A83625	probable transcrip
427	6	1.7	265	2	C95885	probable ionic vol
428	6	1.7	267	2	A64200	DNA polymerase III
429	6	1.7	267	2	JN0831	GlnR protein - Str
430	6	1.7	268	2	F90142	hypothetical prote
431	6	1.7	271	2	T41026	probable methyltra
432	6	1.7	271	2	T08009	probable ribosomal
433	6	1.7	271	2	T49956	hypothetical prote
434	6	1.7	271	2	B72270	conserved hypothet
435	6	1.7	272	2	A71202	probable L-isoaspa
436	6	1.7	273	2	AF2025	hypothetical prote
437	6	1.7	274	2	G97034	probable metal-dep
438	6	1.7	275	2	D70737	hypothetical prote
439	6	1.7	275	2	F69402	conserved hypothet
440	6	1.7	276	2	T45275	oxidoreductase of
441	6	1.7	276	2	D70191	hypothetical prote
442	6	1.7	277	1	A45961	2,5-diketo-D-gluc
443	6	1.7	277	2	C70017	4-hydroxybenzoyl-C
444	6	1.7	278	2	D47055	streptomycin resis
445	6	1.7	278	2	JH0124	streptomycin resis
446	6	1.7	278	2	I51344	dnak-type molecula
447	6	1.7	278	2	C83552	hypothetical prote
448	6	1.7	278	2	AG2176	hypothetical prote
449	6	1.7	279	2	F86842	prephenate dehydra
450	6	1.7	279	2	A89920	conserved hypothet
451	6	1.7	281	2	C69588	L-arabinose transp
452	6	1.7	281	2	E75330	degV protein - Dei
453	6	1.7	281	2	B86896	hypothetical prote
454	6	1.7	281	2	T03509	probable arsenate
455	6	1.7	281	2	C97649	probable ATP-bind1
456	6	1.7	283	2	H95194	hypothetical prote
457	6	1.7	283	2	E98061	conserved hypothet
458	6	1.7	284	2	D81199	conserved hypothet
459	6	1.7	284	2	D81834	conserved hypothet
460	6	1.7	284	2	AD3184	pirin-like protein
461	6	1.7	284	2	H83119	probable transcrip
462	6	1.7	284	2	T39544	suppressor protein
463	6	1.7	284	2	S27931	Env/v-mpl fusion p
464	6	1.7	285	2	F82957	hypothetical prote
465	6	1.7	286	2	G97710	stage 0 sporulatio
466	6	1.7	286	2	F82082	transcription regu
467	6	1.7	287	2	S57770	xyloglucan endo-1,
468	6	1.7	287	2	T22324	hypothetical prote
469	6	1.7	287	2	T42085	MPT4 protein homol
470	6	1.7	288	2	H64453	hypothetical prote
471	6	1.7	289	2	E87708	glutamate racemase
472	6	1.7	289	2	S49812	xyloglucan endo-1,
473	6	1.7	290	2	AG2347	prephenate dehydra
474	6	1.7	290	2	T18992	hypothetical prote
475	6	1.7	290	2	T18706	hypothetical prote
476	6	1.7	291	2	F70463	methylenetetrahydr
477	6	1.7	292	1	A39871	calponin alpha, sm
478	6	1.7	293	2	A40644	transcription regu
479	6	1.7	293	2	A83055	probable aminoacyl
480	6	1.7	294	2	JC5305	hypothetical prote
481	6	1.7	295	2	A40587	probable transcrip
482	6	1.7	295	2	D69534	conserved hypothet
483	6	1.7	296	1	S31483	calponin H2 - pig
484	6	1.7	296	1	D82658	hypothetical prote
485	6	1.7	297	2	JN0773	calponin H1 - rat
486	6	1.7	297	1	S31484	calponin H1 - pig
487	6	1.7	297	1	S31486	calponin H1 - mous
488	6	1.7	297	2	JC4500	basic calponin - h
489	6	1.7	297	2	G02142	smooth muscle cell
490	6	1.7	297	2	C83285	probable transcrip
491	6	1.7	297	2	S76306	hypothetical prote
492	6	1.7	298	2	H83863	modulation of Chea
493	6	1.7	298	2	B35272	osteoinductive fac
494	6	1.7	298	2	JC4130	osteoglycin precu
495	6	1.7	299	2	A35272	osteoinductive fac
496	6	1.7	300	2	S41171	transrepressor pro
497	6	1.7	300	2	AC0678	probable membrane
498	6	1.7	300	2	I39495	probable nitroge
499	6	1.7	300	2	A69351	heterodisulfide re
500	6	1.7	301	2	S76574	hypothetical prote
501	6	1.7	301	2	AB0161	FecCD transport fa
502	6	1.7	301	2	H71011	probable thiamin b
503	6	1.7	302	2	A70599	hypothetical prote
504	6	1.7	302	2	S27846	hypothetical prote
505	6	1.7	303	2	D85356	cinnamoyl-CoA redu
506	6	1.7	304	2	D81445	branched-chain-aml
507	6	1.7	304	2	T13380	ribokinase homolog
508	6	1.7	305	1	S31485	calponin H2 - mous
509	6	1.7	305	2	A31562	guanine nucleotide
510	6	1.7	305	2	T02851	probable membrane
511	6	1.7	305	2	T49783	hypothetical prote
512	6	1.7	305	2	F82303	ABC transporter, A
513	6	1.7	306	2	H90740	hypothetical prote
514	6	1.7	306	2	C64819	yibS protein precu
515	6	1.7	306	2	C85591	hypothetical prote
516	6	1.7	306	2	G95364	probable ABC trans
517	6	1.7	307	1	KISM6C	streptomycin 6-kin
518	6	1.7	307	2	G97575	probable permease
519	6	1.7	307	2	AG2796	hypothetical prote
520	6	1.7	308	2	S76000	hypothetical prote
521	6	1.7	308	2	F70917	probable integral m
522	6	1.7	308	2	C95935	probable sulfoctan
523	6	1.7	309	2	JC4906	calponin - human
524	6	1.7	310	2	H75153	chiamin monophosph
525	6	1.7	310	2	C70871	hypothetical prote
526	6	1.7	310	2	H70792	hypothetical prote
527	6	1.7	311	2	A98304	oligopeptide ABC c
528	6	1.7	311	2	AD2979	hypothetical prote
529	6	1.7	311	2	T11017	MCL536.34 protein
530	6	1.7	311	2	A99933	hypothetical prote
531	6	1.7	312	2	A70708	hypothetical prote
532	6	1.7	313	2	S59448	hypothetical prote
533	6	1.7	313	2	H87731	protein W10C8.1 [i
534	6	1.7	315	2	B69397	conserved hypothet
535	6	1.7	315	2	F90589	conserved hypothet
536	6	1.7	316	2	F64182	cysteine synthase
537	6	1.7	316	2	A57036	olfactory receptor
538	6	1.7	317	2	A47336	R-phycocerythrin ga
539	6	1.7	317	2	D70617	hypothetical prote
540	6	1.7	318	2	T02288	hypothetical prote

541	6	1.7	318	2	G87342	hypothetical prote	614	6	1.7	343	2	A41748	lumican precursor
542	6	1.7	319	2	S30173	probable mercuric	615	6	1.7	343	2	T26594	hypothetical prote
543	6	1.7	320	2	A95266	probable ABC trans	616	6	1.7	343	2	S03415	hypothetical prote
544	6	1.7	321	2	G95920	probable epimerase	617	6	1.7	343	2	E86198	hypothetical prote
545	6	1.7	321	2	G81404	UDP-3-O-(3-hydroxy	618	6	1.7	344	2	C82835	anthranilate phosp
546	6	1.7	322	2	A83549	conserved hypothet	619	6	1.7	344	2	T00110	integral membrane
547	6	1.7	322	2	A97030	membrane protease	620	6	1.7	345	2	T12359	NADH2 dehydrogenas
548	6	1.7	322	2	T12093	TGACG-motif bindin	621	6	1.7	345	2	H72488	probable anthranil
549	6	1.7	322	2	C70700	hypothetical prote	622	6	1.7	345	2	A70664	hypothetical prote
550	6	1.7	322	2	T04595	hypothetical prote	623	6	1.7	345	2	T35357	hypothetical prote
551	6	1.7	322	2	E70326	conserved hypothet	624	6	1.7	345	2	AG3399	plix protein (limpo
552	6	1.7	323	2	D85526	probable permease	625	6	1.7	346	2	T45551	NADH2 dehydrogenas
553	6	1.7	323	2	A99676	probable permease	626	6	1.7	347	2	T17074	NADH2 dehydrogenas
554	6	1.7	323	2	E69177	conserved hypothet	627	6	1.7	347	2	I38008	melanoma antigen M
555	6	1.7	323	2	A72508	probable cobalamin	628	6	1.7	347	2	D83554	hypothetical prote
556	6	1.7	325	1	QOEBB4	UL76 protein - hum	629	6	1.7	347	2	AB3121	oxidoreductase moc
557	6	1.7	325	2	A69184	UDP-glucose 4-epim	630	6	1.7	348	2	H95910	conserved hypothet
558	6	1.7	325	2	H84230	transcription init	631	6	1.7	348	2	F69016	sensory transducti
559	6	1.7	325	2	S59834	probable protein p	632	6	1.7	348	2	D70543	probable nada prot
560	6	1.7	326	2	T08591	TGACG-motif bindin	633	6	1.7	349	2	S30143	alternative respir
561	6	1.7	326	2	A86411	protein F3M18.6 [i	634	6	1.7	349	2	A39158	alternative respir
562	6	1.7	326	2	AD2936	polymerase epsilon	635	6	1.7	349	2	AD0990	WD repeat protein
563	6	1.7	326	2	C98346	hypothetical prote	636	6	1.7	349	2	AE2568	hypothetical prote
564	6	1.7	327	2	T50744	spheroidene monox	637	6	1.7	349	2	AE1923	c-type cytochrome
565	6	1.7	327	2	S49619	cirA protein - Rho	638	6	1.7	350	2	E87714	protein kinase A (
566	6	1.7	327	2	F83408	hypothetical prote	639	6	1.7	351	2	S19027	protein kinase A (
567	6	1.7	327	2	G96833	hypothetical prote	640	6	1.7	352	2	S19028	iron (III)-transpor
568	6	1.7	327	2	T34666	probable regulator	641	6	1.7	352	2	AF3580	deoxyhypusine synt
569	6	1.7	328	2	I51215	inhibin alpha-subu	642	6	1.7	353	2	T51022	deoxyhypusine synt
570	6	1.7	328	2	S69715	hypothetical prote	643	6	1.7	353	2	T47195	probable ATP-bindi
571	6	1.7	328	1	G84826	threonine ammonia-	644	6	1.7	353	2	AI0670	cruciform-cutting
572	6	1.7	329	2	D85973	threonine ammonia-	645	6	1.7	353	2	AB3650	iron (III)-transpor
573	6	1.7	329	2	E91128	2-hydroxyglutaryl-	646	6	1.7	353	2	E88142	hypothetical prote
574	6	1.7	329	2	D69494	acidic calponin -	647	6	1.7	353	2	AF3145	hypothetical prote
575	6	1.7	329	2	UC4501	structural protein	648	6	1.7	353	2	B95885	probable iron ABC
576	6	1.7	329	2	S32582	calponin, acidic -	649	6	1.7	353	2	B75400	phosphoribosylform
577	6	1.7	330	2	A53742	probable secretion	650	6	1.7	354	2	T39599	conserved hypothet
578	6	1.7	330	2	AH0697	hypothetical prote	651	6	1.7	354	2	B91264	phosphonate metabo
579	6	1.7	330	2	S76408	probable secreted	652	6	1.7	354	2	T06748	phosphonate metabo
580	6	1.7	331	2	T35100	probable phytone	653	6	1.7	354	2	B65219	phni protein - Ebc
581	6	1.7	331	2	T36969	conserved hypothet	654	6	1.7	356	2	T51480	hypothetical prote
582	6	1.7	331	2	E83368	deacetoxycephalosp	655	6	1.7	356	2	C96705	probable zinc fing
583	6	1.7	331	2	A29711	pyruvate formate-1	656	6	1.7	356	2	T27338	hypothetical prote
584	6	1.7	332	2	H69494	lipoprotein (impor	657	6	1.7	356	2	T28084	hypothetical prote
585	6	1.7	332	2	AF0407	hypothetical prote	658	6	1.7	356	2	I55210	tricarboxylate car
586	6	1.7	333	2	H83364	cell division prot	659	6	1.7	357	2	A82206	protein-glutamate
587	6	1.7	333	2	AD3261	protein-glutamate	660	6	1.7	357	2	AC0875	conserved hypothet
588	6	1.7	334	2	A36707	aliphatic amidase	661	6	1.7	358	2	A75561	fructose 1,6-bisph
589	6	1.7	334	2	F64674	oligopeptide trans	662	6	1.7	358	2	E83262	hypothetical prote
590	6	1.7	334	2	C71842	Y box-binding prot	663	6	1.7	359	2	T47187	probable glycosylt
591	6	1.7	334	2	T45277	ABC transporter, A	664	6	1.7	359	2	A25732	inhibin alpha chai
592	6	1.7	335	2	B38274	hypothetical prote	665	6	1.7	359	2	T03373	probable G-box bin
593	6	1.7	336	1	A95213	ABC transport syst	666	6	1.7	360	1	E72467	probable non speci
594	6	1.7	336	2	B98077	alcohol dehydrogen	667	6	1.7	360	2	T27504	hypothetical prote
595	6	1.7	336	2	F81348	probable LPS biosy	668	6	1.7	361	2	A53860	phosphate carrier
596	6	1.7	337	1	A42654	probable LPS biosy	669	6	1.7	361	2	T40857	chondroadherin pre
597	6	1.7	337	2	F91191	probable oxidoredu	670	6	1.7	361	2	JQ0735	hypothetical prote
598	6	1.7	337	2	G86038	riboseomal large su	671	6	1.7	362	1	T26520	recf protein - Pro
599	6	1.7	337	2	AG0230	tagatose-1,6-dipho	672	6	1.7	362	2	A53737	hypothetical prote
600	6	1.7	338	2	C75353	hypothetical prote	673	6	1.7	362	2	B43680	K'362 protein - Af
601	6	1.7	338	2	AD1142	hypothetical prote	674	6	1.7	363	2	B87571	hypothetical prote
602	6	1.7	338	2	AD3052	hypothetical prote	675	6	1.7	363	2	T16755	inhibin alpha chai
603	6	1.7	338	2	H98233	hypothetical prote	676	6	1.7	364	1	EDBESP	immediate-early pr
604	6	1.7	339	2	D72509	latency-related pr	677	6	1.7	364	2	I45915	hypothetical prote
605	6	1.7	340	1	WMBE11	hypothetical prote	678	6	1.7	364	2	C86015	hypothetical prote
606	6	1.7	340	2	T20101	hypothetical prote	679	6	1.7	364	2	F90672	probable fructose
607	6	1.7	340	2	E69544	hypothetical prote	680	6	1.7	364	2	T24657	chromoxane A2 rec
608	6	1.7	341	2	E96019	probable sugar upt	681	6	1.7	364	2		
609	6	1.7	341	2	D75479	hypothetical prote	682	6	1.7	364	2		
610	6	1.7	341	2	F81276	probable fructose	683	6	1.7	364	2		
611	6	1.7	343	2	T36539		684	6	1.7	364	2		
612	6	1.7	343	2	A49117		685	6	1.7	364	2		
613	6	1.7	343	2			686	6	1.7	364	2		

687	6	1.7	365	2	A75375	hypothetical prote	760	6	1.7	386	2	A70740	probable fadE14 pr
688	6	1.7	365	1	A24248	inhibin alpha chai	761	6	1.7	386	2	G71467	probable succinyl-
689	6	1.7	366	1	A40056	inhibin alpha chai	762	6	1.7	387	2	I50703	transcription fact
690	6	1.7	366	1	JC1106	env polypeptide -	763	6	1.7	387	2	S46123	hypothetical prote
691	6	1.7	366	2	B41565	conserved hypothet	764	6	1.7	388	2	A75321	prepilin peptidase
692	6	1.7	366	2	D83224	hypothetical prote	765	6	1.7	389	2	T50078	hypothetical prote
693	6	1.7	366	2	D75167	CT338 hypothetical	766	6	1.7	389	2	F72554	hypothetical prote
694	6	1.7	366	2	H86614	conserved hypothet	767	6	1.7	390	2	T35509	hypothetical prote
695	6	1.7	366	2	C72009	iron (iii) abc tra	768	6	1.7	392	2	AD0420	phnI protein (limp
696	6	1.7	366	2	A75077	hypothetical prote	769	6	1.7	392	2	T19327	hypothetical prote
697	6	1.7	367	2	C70820	myb protein - rice	770	6	1.7	393	1	S42068	mitogen-activated
698	6	1.7	367	2	PB0401	probable C-P (carb	771	6	1.7	393	2	T33917	hypothetical prote
699	6	1.7	368	2	T03828	a Nifs-like protei	772	6	1.7	394	2	E72519	similar to amidase
700	6	1.7	368	2	AF1327	probable C-P (carb	773	6	1.7	394	2	B50007	hypothetical prote
701	6	1.7	368	2	E96023	ankyrin repeat pro	774	6	1.7	394	2	F72517	lipid-A-disacchari
702	6	1.7	368	2	T18184	two-component sens	775	6	1.7	395	2	AE3356	hypothetical prote
703	6	1.7	368	2	D83823	thromboxane A-2 re	776	6	1.7	395	2	E98166	moca protein (limp
704	6	1.7	369	2	A53959	dnau protein - The	777	6	1.7	396	2	A70581	hypothetical prote
705	6	1.7	369	2	B72327	conserved hypothet	778	6	1.7	396	2	A70581	hypothetical prote
706	6	1.7	369	2	AE2598	phnI protein (limp	779	6	1.7	397	2	S49301	AWJ1175 protein -
707	6	1.7	369	2	F97380	conserved hypothet	780	6	1.7	397	2	A69135	bacteriochlorophyl
708	6	1.7	369	2	AG0625	hypothetical prote	781	6	1.7	397	2	T66119	hypothetical prote
709	6	1.7	369	2	G90757	hypothetical prote	782	6	1.7	397	2	AF2016	hypothetical prote
710	6	1.7	369	2	B85523	hypothetical prote	783	6	1.7	398	2	T05873	hypothetical prote
711	6	1.7	369	2	E85621	hypothetical prote	784	6	1.7	399	2	F72417	MFS permease (drug
712	6	1.7	369	2	B64835	probable iron-sulf	785	6	1.7	399	2	AC2785	hypothetical prote
713	6	1.7	370	2	A69430	conserved hypothet	786	6	1.7	399	2	D97564	homoserine O-acety
714	6	1.7	370	2	E83848	aminotransferase (787	6	1.7	401	2	G84392	porphobilinogen sy
715	6	1.7	371	2	S77345	hypothetical prote	788	6	1.7	401	2	S16738	conserved hypothet
716	6	1.7	371	2	C83991	hypothetical prote	789	6	1.7	401	2	C82660	connexin44 - bovin
717	6	1.7	371	2	E72665	hypothetical prote	790	6	1.7	402	2	I46053	glutaryl-tRNA redu
718	6	1.7	372	2	F97510	BA483f11.2.1 (cox1	791	6	1.7	404	2	T45026	probable nitrogen
719	6	1.7	373	2	A57559	3beta-hydroxy-Delt	792	6	1.7	404	2	C71303	probable type-III
720	6	1.7	373	2	JC4162	P2Y receptor - bov	793	6	1.7	405	2	AD0032	multidrug resistan
721	6	1.7	373	2	JQ1648	SHL2 protein - hum	794	6	1.7	405	2	AE3649	hypothetical prote
722	6	1.7	373	2	T47396	hypothetical prote	795	6	1.7	405	2	E72521	ceoA protein - Bur
723	6	1.7	374	1	F70584	phosphate specific	796	6	1.7	405	2	T43023	hypothetical prote
724	6	1.7	375	2	S05390	fibromodulin precu	797	6	1.7	406	2	AE2455	mRNA binding prote
725	6	1.7	375	2	AH3110	oxoreductase (limp	798	6	1.7	406	2	T48103	hydroxyneurosporen
726	6	1.7	375	2	D98176	hypothetical prote	799	6	1.7	406	2	T50894	Na+/H+ exchange pr
727	6	1.7	376	1	KIBE17	thymidine kinase (800	6	1.7	406	2	B82686	probable thromboxa
728	6	1.7	376	1	KIBET	thymidine kinase (801	6	1.7	407	2	T02670	glucose/galactose
729	6	1.7	376	1	KIBE16	thymidine kinase (802	6	1.7	407	2	F44666	glucose/galactose
730	6	1.7	376	1	KIBEHF	thymidine kinase (803	6	1.7	407	2	A71850	hypothetical prote
731	6	1.7	376	1	KIBEKS	thymidine kinase (804	6	1.7	407	2	T19895	leucyl aminopeptid
732	6	1.7	376	1	KIBETC	hypothetical prote	805	6	1.7	408	2	JC5862	endoglucanase B -
733	6	1.7	376	2	H90407	polysaccharide poi	806	6	1.7	409	2	S12018	probable spore coa
734	6	1.7	376	2	AC2189	alpha-N-acetylneur	807	6	1.7	412	2	E71369	activin beta-A cha
735	6	1.7	376	2	S55275	hypothetical prote	808	6	1.7	412	2	C72548	glucose-1-phosphat
736	6	1.7	376	2	JC5600	hypothetical prote	809	6	1.7	413	2	AG6632	glucose-1-phosphat
737	6	1.7	376	2	C91169	hypothetical prote	810	6	1.7	413	2	JV0087	periplasmic glucos
738	6	1.7	376	2	S47693	hypothetical prote	811	6	1.7	413	2	F30773	hemolysin - cecropia
739	6	1.7	376	2	T20972	phenylalanine dehy	812	6	1.7	413	2	B85636	hypothetical prote
740	6	1.7	379	2	B83677	hypothetical prote	813	6	1.7	413	2	S65948	hemolysin - cecropia
741	6	1.7	379	2	B70937	probable protein k	814	6	1.7	413	2	A37778	hypothetical prote
742	6	1.7	379	2	T47507	GumH protein - Xan	815	6	1.7	413	2	T12533	probable acyl-CoA
743	6	1.7	380	2	S67857	cystathionine gamm	816	6	1.7	415	2	D75616	glycoprotein D pre
744	6	1.7	380	2	B64533	factor VIII-associ	817	6	1.7	417	1	VG8E1B	glycophorin GD -
745	6	1.7	380	2	D71973	hypothetical prote	818	6	1.7	417	2	S35784	glucose 6 phosphat
746	6	1.7	380	2	A42832	transforming prote	819	6	1.7	417	2	T51467	hypothetical prote
747	6	1.7	380	2	D82965	ompF-like porin [I	820	6	1.7	417	2	AB1315	conserved hypothet
748	6	1.7	381	1	TVMVJ	hypothetical membr	821	6	1.7	417	2	AB1687	keratin, type I cy
749	6	1.7	381	2	B82653	probable FAD-depen	822	6	1.7	417	2	AE2735	probable sugar upt
750	6	1.7	382	2	G84971	probable dioxygena	823	6	1.7	418	2	S62483	D-amino acid dehyd
751	6	1.7	382	2	E83322	probable NADH dehy	824	6	1.7	420	2	G96002	sugar phosphate nu
752	6	1.7	382	2	E83322	hypothetical prote	825	6	1.7	421	2	F82279	collagen precursor
753	6	1.7	383	2	T36080	hypothetical prote	826	6	1.7	422	2	F90250	ragd protein - Bra
754	6	1.7	383	2	E87680	sugar isomerase -	827	6	1.7	423	2	A55797	hypothetical prote
755	6	1.7	383	2	A72299	hypothetical prote	828	6	1.7	423	2	T13142	hypothetical prote
756	6	1.7	383	2	T08970	probable ABC trans	829	6	1.7	423	2	A99242	
757	6	1.7	384	2	G95950	hypothetical prote	830	6	1.7	423	2	AC3044	
758	6	1.7	384	2	F72567		831	6	1.7	423	2		
759	6	1.7	385	2			832	6	1.7	423	2		

833	6	1.7	424	1	B40905	inhibin beta-A cha	906	6	1.7	448	2	A81369	probable lipoprote
834	6	1.7	424	1	S31440	inhibin beta-A cha	907	6	1.7	449	2	T45605	glucosyltransferas
835	6	1.7	424	1	WFPGBA	inhibin beta-A cha	908	6	1.7	449	2	AD3181	two component sens
836	6	1.7	424	2	B81960	probable inner mem	909	6	1.7	449	2	H70652	hypothetical prote
837	6	1.7	424	2	C70651	hypothetical prote	910	6	1.7	450	2	T43188	hypothetical prote
838	6	1.7	425	1	S50898	inhibin beta-A cha	911	6	1.7	450	2	T40337	probable baccharop
839	6	1.7	425	2	AC3391	tetracenomycin c p	912	6	1.7	450	2	C86262	F13K23.12 protein
840	6	1.7	425	2	I47072	inhibin beta-A cha	913	6	1.7	451	2	B81056	proteinase, probab
841	6	1.7	425	2	G83969	cell-division prot	914	6	1.7	451	2	C81820	probable proteinas
842	6	1.7	425	2	S60446	hypothetical prote	915	6	1.7	451	2	H75593	hypothetical prote
843	6	1.7	425	2	T12473	hypothetical prote	916	6	1.7	452	1	S14332	rhodopsin - northe
844	6	1.7	425	2	B97516	hypothetical prote	917	6	1.7	453	2	T37054	hypothetical prote
845	6	1.7	426	1	B24248	inhibin beta-A cha	918	6	1.7	454	2	T35016	probable 3-carboxy
846	6	1.7	426	2	T51506	hypothetical prote	919	6	1.7	454	2	E70448	signal recognition
847	6	1.7	426	2	A82660	glucose/galactose	920	6	1.7	454	2	T02275	hypothetical prote
848	6	1.7	426	2	A30212	alpha-factor recep	921	6	1.7	454	2	G75105	hypothetical prote
849	6	1.7	427	2	S57898	glutamate-1-semial	922	6	1.7	455	1	JC4338	UDP-N-acetylmutamy
850	6	1.7	427	2	G83149	tetrahydrofolylpol	923	6	1.7	455	2	T31440	hypothetical prote
851	6	1.7	427	2	B86769	Arab protein PA227	924	6	1.7	455	2	H71028	probable two-compo
852	6	1.7	427	2	G83361	glycosyltransferas	925	6	1.7	456	2	F97372	hypothetical prote
853	6	1.7	427	2	AD3149	hypothetical prote	926	6	1.7	456	2	C86624	hypothetical prote
854	6	1.7	427	2	G98138	hypothetical prote	927	6	1.7	456	2	H72000	hypothetical prote
855	6	1.7	428	2	A83807	hypothetical prote	928	6	1.7	457	2	H85059	probable sugar tra
856	6	1.7	429	1	B25937	arsenical pump mem	929	6	1.7	457	2	AF3426	phosphomannomutase
857	6	1.7	429	1	B41902	arsenical pump mem	930	6	1.7	458	2	E71059	probable endo-1,4-
858	6	1.7	429	1	C41903	arsenical pump mem	931	6	1.7	459	2	AC2057	chromosomal replic
859	6	1.7	429	2	F91175	arsenical pump mem	932	6	1.7	459	2	T45576	anthranilate N-hyd
860	6	1.7	429	2	F86021	arsenical pump mem	933	6	1.7	461	2	D89894	hypothetical prote
861	6	1.7	429	2	AE0406	arsenical pump mem	934	6	1.7	462	2	AC0672	nitrite extrusion
862	6	1.7	430	2	G89962	hypothetical prote	935	6	1.7	462	2	S11431	nitrite extrusion
863	6	1.7	430	2	C90696	probable amino aci	936	6	1.7	462	2	A85730	nitrite extrusion
864	6	1.7	430	2	G85546	probable amino aci	937	6	1.7	462	2	H90887	nitrite extrusion
865	6	1.7	430	2	E64779	hypothetical prote	938	6	1.7	463	2	T09243	dnak-type molecule
866	6	1.7	430	2	T45437	arsenic efflux pum	939	6	1.7	464	2	C82967	probable peptidase
867	6	1.7	431	2	AD1237	arsenic efflux pum	940	6	1.7	465	2	T07620	dnak-type molecule
868	6	1.7	431	2	A11599	arsenic efflux pum	941	6	1.7	465	2	JC5184	glutamate synthase
869	6	1.7	432	1	E70373	conserved hypotet	942	6	1.7	466	2	E70865	trigger factor lig
870	6	1.7	432	2	F83525	TolB protein PA097	943	6	1.7	467	2	I50476	keratin type I - g
871	6	1.7	432	2	C95275	probable ABC trans	944	6	1.7	467	2	T45475	heat-shock protein
872	6	1.7	433	2	S01631	keratin, type I, e	945	6	1.7	468	2	S21172	glutamate-tRNA lig
873	6	1.7	433	2	D75352	deoxyguanosinetrip	946	6	1.7	468	2	T45476	heat-shock protein
874	6	1.7	435	2	G69779	arsenical pump mem	947	6	1.7	468	2	H70427	replicative DNA he
875	6	1.7	435	2	T46643	hypothetical prote	948	6	1.7	468	2	G82329	heat-shock protein
876	6	1.7	436	2	B55452	cartilage-derived	949	6	1.7	469	2	T45478	replicative DNA he
877	6	1.7	436	2	G84024	arsenic efflux pum	950	6	1.7	469	2	T34645	heat-shock protein
878	6	1.7	436	2	S47723	arsenite efflux pum	951	6	1.7	469	2	S36536	hypothetical prote
879	6	1.7	436	2	T36104	conserved hypotet	952	6	1.7	470	2	E75085	l2 protein - human
880	6	1.7	437	2	H84865	probable sterol de	953	6	1.7	470	2	F96806	transmembrane tran
881	6	1.7	438	2	T45602	glucosyltransferas	954	6	1.7	471	2	B97433	probable AUX1-like
882	6	1.7	438	2	B84919	Not56-like protein	955	6	1.7	471	2	AC2651	hypothetical prote
883	6	1.7	439	2	H70582	probable transposa	956	6	1.7	471	2	T121972	transcription regu
884	6	1.7	439	2	B86302	hypothetical prote	957	6	1.7	472	2	S76290	hypothetical prote
885	6	1.7	439	2	S51378	probable membrane	958	6	1.7	472	2	A31082	ribulose-bisphosph
886	6	1.7	439	2	G97159	contains cell adhe	959	6	1.7	472	2	T27754	hypothetical prote
887	6	1.7	440	1	S60755	rhodopsin - Allote	960	6	1.7	473	2	C64371	aspartate kinase (
888	6	1.7	441	2	S14441	retinol-binding pr	961	6	1.7	473	2	H72419	virulence factor M
889	6	1.7	441	2	C83318	conserved hypotet	962	6	1.7	473	2	T19707	hypothetical prote
890	6	1.7	441	2	T23461	hypothetical prote	963	6	1.7	475	2	C71404	hypothetical prote
891	6	1.7	442	2	A71486	probable yop N (fl	964	6	1.7	475	2	C96503	protein F9C16.7 (l
892	6	1.7	442	2	B82633	nitrite hydratase	965	6	1.7	475	2	D64799	probable enzyme of
893	6	1.7	442	2	T38691	hypothetical prote	966	6	1.7	475	2	A85565	probable enzyme of
894	6	1.7	442	2	D87351	conserved hypotet	967	6	1.7	475	2	D90714	hypothetical prote
895	6	1.7	442	2	S50062	cell wall glycopro	968	6	1.7	475	2	T26850	hypothetical prote
896	6	1.7	444	2	C81054	phosphoglucmutase	969	6	1.7	476	2	S09152	translactation elonga
897	6	1.7	444	2	C81823	probable phosphogl	970	6	1.7	477	2	H86619	shikimate 5-dehydro
898	6	1.7	444	2	B95065	conserved hypotet	971	6	1.7	477	2	G72003	3-dehydroquinatate d
899	6	1.7	444	2	F97932	conserved hypotet	972	6	1.7	477	2	H83389	hypothetical prote
900	6	1.7	445	2	S48696	suppressor protein	973	6	1.7	478	2	S47040	gene Tt52 protein
901	6	1.7	445	2	T24723	hypothetical prote	974	6	1.7	479	2	H83590	dhhydropyrimidinase
902	6	1.7	446	2	G81326	probable DNA repai	975	6	1.7	479	2	T23508	hypothetical prote
903	6	1.7	446	2	T51368	sterile apetala lv	976	6	1.7	479	2	G75092	asparagine synthas
904	6	1.7	447	2	T12978	hypothetical prote	977	6	1.7	480	2	F72205	alpha-glucosidase
905	6	1.7	448	2	A83590	two component resp	978	6	1.7	480	2	JC7866	endo-1,6-beta-D-gl

979	6	1.7	482	2	G75483	probable leucyl am
980	6	1.7	482	2	JH0110	arginine/ornithine
981	6	1.7	483	2	E84596	AUX1-like amino ac
982	6	1.7	485	2	S03834	hypothetical prote
983	6	1.7	486	2	T51431	glucosyltransferas
984	6	1.7	487	2	B83095	UDP-N-acetylmutamo
985	6	1.7	487	2	AE0488	probable membrane
986	6	1.7	488	1	QXASM4	NADH2 dehydrogenas
987	6	1.7	488	2	D70876	probable polyketid
988	6	1.7	488	2	C75488	argininosuccinate
989	6	1.7	488	2	A27353	collagen alpha 1(I
990	6	1.7	488	2	I56507	histamine H1 recep
991	6	1.7	488	2	C41977	retinoid receptor
992	6	1.7	488	2	T45964	LAX1 / AUX1-like p
993	6	1.7	490	2	T23791	hypothetical prote
994	6	1.7	491	2	A40283	3',5'-cyclic-nucle
995	6	1.7	492	2	A81852	probable type III
996	6	1.7	493	2	F84689	probable cytochrom
997	6	1.7	493	2	G84689	probable cytochrom
998	6	1.7	493	2	T10054	pyruvate kinase (E
999	6	1.7	493	2	I49370	plasma phospholipi
1000	6	1.7	493	2	T48934	acyl CoA reductase

ALIGNMENTS

RESULT 1

JC5241

activin beta E chain precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C/Accession: JC5241; JC5367

R/Fang, J.; Yin, W.; Smiley, E.; Wang, S.Q.; Bonadio, J.

Biochem. Biophys. Res. Commun. 228, 669-674, 1996

A/Title: Molecular cloning of the mouse activin beta E subunit gene.

A/Reference number: JC5241; MUID:97096313; PMID:8941337

A/Contents: liver

A/Accession: JC5241

A/Molecule type: mRNA

A/Residues: 1-350 <FAN>

A/Cross-references: UNIPROT:O08717; GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g20725

R/Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.

Biochem. Biophys. Res. Commun. 231, 655-661, 1997

A/Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit

A/Reference number: JC5366; MUID:97224404; PMID:9070865

A/Accession: JC5367

A/Molecule type: DNA

A/Residues: 1-350 <FAN>

A/Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522

C/Genetics:

A/Introns: 99/3

C/Superfamily: inhibin

Query Match 19.1%; Score 67; DB 2; Length 350;

Best Local Similarity 100.0%; Pred.No. 8.6e-58;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 TPLCGRDHYVDFQELGWRDWILOPEGYQLNYCSGQCPHLAGSPGIAASFHSAVLSLK 303

Db 244 TPLCGRDHYVDFQELGWRDWILOPEGYQLNYCSGQCPHLAGSPGIAASFHSAVLSLK 303

QY 304 ANNPWPA 310

Db 304 ANNPWPA 310

RESULT 2

JC2466

inhibin beta-C chain precursor - human

N/Alternate names: activin beta C chain

C/Species: Homo sapiens (man)

C/Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C/Accession: JC2466
R/Hoetten, G.; Neidhardt, H.; Schneider, C.; Pohl, J.
Biochem. Biophys. Res. Commun. 206, 608-613, 1995
A/Title: Cloning of a new member of the TGF-beta family: A putative new activin beta C.
A/Reference number: JC2466; MUID:95126961; PMID:7826378
A/Accession: JC2466
A/Molecule type: mRNA
A/Residues: 1-352 <HOE>
A/Cross-references: UNIPROT:P55103; GB:X82540; NID:g669154; PIDN:CAA57890.1; PID:g66915
A/Experimental source: liver
C/Genetics:
A/Gene: GDB:INHBC
A/Cross-references: GDB:632884
A/Map position: 2cen-2q13
C/Superfamily: inhibin
C/Keywords: glycoprotein
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-236/Domain: propeptide #status predicted <PRO>
F/237-352/Product: activin beta C #status predicted <MAT>
F/110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 4.3%; Score 15; DB 2; Length 352;

Best Local Similarity 100.0%; Pred.No. 1.5e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 SCCVPTARRPLSLY 327

Db 315 SCCVPTARRPLSLY 329

RESULT 3

S70580

activin beta C precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S70580

R/Lau, A.L.; Nishimori, K.; Matzuk, M.M.

Biochim. Biophys. Acta 1307, 145-148, 1996

A/Title: Structural analysis of the mouse activin beta-C gene.

A/Reference number: S70580; MUID:96283807; PMID:8679697

A/Accession: S70580

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-352 <LAU>

A/Cross-references: UNIPROT:P55104; EMBL:U40772

C/Genetics:

A/Introns: 106/1

C/Superfamily: inhibin

Query Match 3.1%; Score 11; DB 2; Length 352;

Best Local Similarity 100.0%; Pred.No. 0.013;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 PDMVEACGCS 350

Db 342 PDMVEACGCS 352

RESULT 4

JC5366

activin beta C - mouse

C/Species: Mus musculus (house mouse)

C/Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004

C/Accession: JC5366

R/Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.

Biochem. Biophys. Res. Commun. 231, 655-661, 1997

A/Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibi

A/Reference number: JC5366; MUID:97224404; PMID:9070865

A/Accession: JC5366

A/Molecule type: DNA

A/Residues: 1-352 <FAN>

A/Cross-references: UNIPROT:P55104; GB:U95962

C/Comment: Activin beta C and beta E form a distinct subset of related activins.

C/Genetics:
A/Introns: 105/3
C/Superfamily: inhibin

Query Match 3.1%; Score 11; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 PDMVVEACGCS 350
|||||
Db 342 PDMVVEACGCS 352

RESULT 5
S43296
bone morphogenetic protein-related protein (GDF7) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S43296
R/Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A/Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
A/Reference number: S43294; MUID:94195427; PMID:8145850
A/Accession: S43296
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-151 <STO>
A/Cross-references: UNIPROT:P43029; GB:U08339; NID:G488465; PIDN:AAA18780.1; PID:G488466
C/Superfamily: inhibin

Query Match 2.6%; Score 9; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 DMVVEACGC 349
|||||
Db 142 DMVVEACGC 150

RESULT 6

T14455
hypothetical protein - wild cabbage (fragment)
C/Species: Brassica oleracea (wild cabbage)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14455
R/Croy, R.D.; Booker, J.P.
submitted to the EMBL Data Library, July 1996
A/Reference number: Z18098
A/Accession: T14455
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-283 <CRO>
A/Cross-references: UNIPROT:Q39374; EMBL:Z74841; NID:el001204; PID:e256042
A/Experimental source: strain albolabura; atigma

Query Match 2.3%; Score 8; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 KIRANEPG 229
|||||
Db 193 KIRANEPG 200

RESULT 7

D86425
unknown protein (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D86425
R/Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000.

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Malt, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: D86425
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-311 <STO>
A/Cross-references: UNIPROT:Q9CGZ4; GB:AE005172; NID:G11094785; PIDN:AAG29717.1; GSPDB:
C/Genetics:
A/Map position: 1

Query Match 2.3%; Score 8; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 KIRANEPG 229
|||||
Db 175 KIRANEPG 182

RESULT 8

JC4151
activin beta D chain precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: JC4151
R/Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 210, 581-588, 1995
A/Title: Molecular cloning and functional analysis of a new activin beta subunit: a dcr
A/Reference number: JC4151; MUID:95275314; PMID:7755637
A/Accession: JC4151
A/Molecule type: mRNA
A/Residues: 1-367 <ODA>
A/Cross-references: UNIPROT:Q91696; DDBJ:D49543; NID:G961512; PIDN:BAA08494.1; PID:G961
A/Experimental source: embryo
C/Superfamily: inhibin
C/Keywords: glycoprotein; mesoderm
F/1-253/Domain: signal sequence #status predicted <SIG>
F/254-367/Product: activin beta D chain #status predicted <MAT>
F/64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.3%; Score 8; DB 2; Length 367;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ELAKQITL 52
|||||
Db 47 ELAKQITL 54

RESULT 9

S22701
mannosyltransferase (EC 2.4.1.-) - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein G3626; protein YGL038c
C/Species: Saccharomyces cerevisiae
C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C/Accession: S22701; S64040
R/Nakayama, K.I.; Nagasu, T.; Shima, Y.; Kuromitsu, J.; Uigami, Y.
EMBO J. 11, 2511-2519, 1992
A/Title: OCH1 encodes a novel membrane bound mannosyltransferase: outer chain elongatio
A/Reference number: S22701; MUID:92331603; PMID:1628616
A/Accession: S22701
A/Molecule type: DNA
A/Residues: 1-480 <NAK>
A/Cross-references: UNIPROT:P31755; EMBL:D11095; NID:G218450; PIDN:BAA01869.1; PID:G218
R/Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64003

A/Accession: S64040
A/Molecule type: DNA
A/Residues: 1-480 <HEB>
A/Cross-references: EMBL:Z72560; NID:G1322519; PID:e243938; PID:G1322520; MIPS:YGL038C
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:OCH1
A/Cross-references: SGD:S0003006; MIPS:YGL038C
A/Map position: 7L
C/Keywords: glycoprotein, glycosyltransferase, hexosyltransferase, transmembrane protein
F:16-32/Domain: transmembrane #status predicted <TM>
F:203,281,341,393/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.3%; Score 8; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 SLTFHLS 114
|||
Db 26 SLTFHLS 33

RESULT 10
Serrine proteinase (EC 3.4.21.-) precursor - Serratia marcescens (strain IFO-3046)
C/Species: Serratia marcescens
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C/Accession: A29840
R/Yanagida, N.; Uozumi, T.; Bepu, T.
J. Bacteriol. 166, 937-944, 1986
A/Title: Specific excretion of Serratia marcescens protease through the outer membrane
A/Reference number: A29840; MUID:86223815; PMID:3011754
A/Accession: A29840
A/Molecule type: DNA
A/Residues: 1-1045 <YAN>
A/Cross-references: UNIPROT:P09489; GB:M13469; NID:G152857; PIDN:AAA26572.1; PID:G152858
C/Superfamily: autotransporter subtilisin-like protease precursor; subtilisin homology
C/Keywords: hydrolase, serine proteinase
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-408/Product: serine proteinase #status predicted <MAT>
F:67-355/Domain: subtilisin homology <SBT>
F:409-1045/Domain: carboxyl-terminal propeptide #status predicted <PRO>
F:76,112,341/Active site: Asp, His, Ser #status predicted

Query Match 2.3%; Score 8; DB 2; Length 1045;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 GSVAPGNG 89
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Db 525 GSVAPGNG 532

RESULT 11
S63993
acrosomal protein AZ1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C/Accession: S63993; S63992
R/Aoto, H.; Tsuchida, J.; Nishina, Y.; Nishimune, Y.; Abano, A.; Tajima, S.
Submitted to the EMBL Data Library, December 1994
A/Description: Isolation of a novel cDNA that encodes a protein localized to the pre-acr
A/Reference number: S63993
A/Accession: S63993
A/Molecule type: mRNA
A/Residues: 1-1060 <AOT>
A/Cross-references: UNIPROT:Q62036; EMBL:D43921; NID:G1827501; PIDN:BAA07868.1; PID:d100
A/Note: this is a revision to the sequence from reference S63992
R/Aoto, H.; Tsuchida, J.; Nishina, Y.; Nishimune, Y.; Abano, A.; Tajima, S.
Eur. J. Biochem. 234, 8-15, 1995
A/Title: Isolation of a novel cDNA that encodes a protein localized to the pre-acrosome
A/Reference number: S63992; MUID:96096715; PMID:8529672
A/Accession: S63992

A/Molecule type: mRNA
A/Residues: 1-942, 'SGCSP' <AOW>
A/Cross-references: EMBL:D43921
A/Note: this sequence has been revised in reference S63993

Query Match 2.3%; Score 8; DB 2; Length 1060;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 AALTRALR 77
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Db 807 AALTRALR 814

RESULT 12
E72611
probable ATP-dependent DNA helicase APE1353 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: E72611
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Take
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A/Accession: E72611
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1273 <KAW>
A/Cross-references: UNIPROT:Q9YCA1; DDBJ:AP000061; NID:G5104821; PIDN:BAA80347.1; PID:d
A/Experimental source: strain K1
C/Genetics:
A/Gene: APE1353

Query Match 2.3%; Score 8; DB 2; Length 1273;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 176 SGLRGEKS 183
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Db 1121 SGLRGEKS 1128

RESULT 13
S28793
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments)
N/Alternate names: major surface antigen p190
C/Species: Plasmodium falciparum
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C/Accession: S28793
R/Hall, R.; Hyde, J.E.; Goman, M.; Simmons, D.L.; Hope, I.A.; Mackay, M.; Scaife, J.; M
Nature 311, 379-382, 1984
A/Title: Major surface antigen gene of a human malaria parasite cloned and expressed in
A/Reference number: S28793; MUID:85012680; PMID:6090934
A/Accession: S28793
A/Molecule type: mRNA
A/Residues: 1-72 <HAL>
A/Cross-references: UNIPROT:Q25925; EMBL:M32152; NID:G160423; PIDN:AAA29658.1; PID:G160
C/Superfamily: major merozoite surface antigen
C/Keywords: merozoite, surface antigen

Query Match 2.0%; Score 7; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 LKIRANE 227
|||
Db 26 LKIRANE 32

RESULT 14
G84229
hypothetical protein Vng0724h [imported] - Halobacterium sp. NRC-1

C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: G84229
R/NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: A84160, MUID:20504483; PMID:11016950
A/Accession: G84229
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-86 <STO>
A/Cross-references: UNIPROT:Q9HRF5; GB:AE004437; NID:g10580303; PIDN:AAG19203.1; GSPDB:C
C/Genetics:
A/Gene: VNG0724H

Query Match 2.0%; Score 7; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 ARRLSL 325
|||
DB 12 ARRLSL 18

RESULT 15

AH3212
hypothetical protein Atus431 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AH3212
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AH3212
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-129 <KUR>
A/Cross-references: UNIPROT:Q8UJP5; GB:AE008687; PIDN:AAL46118.1; PID:g17743884; GSPDB:C
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: Atus431
A/Genome: plasmid

Query Match 2.0%; Score 7; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 RTLLAEH 161
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DB 24 RTLLAEH 30

Search completed: October 13, 2005, 18:47:17
Job time : 80 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2005, 18:38:45 ; Search time 43 Seconds
(without alignments)
607.609 Million cell updates/sec

Title: US-10-666-225-14

Perfect score: 350

Sequence: 1 MRUPDVQLMLVLMALVRAQ.....NGNVKTDVDPDMVEACGCS 350

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	350	100.0	350	2	US-08-765-662-14
2	350	100.0	350	5	PCT-US95-08745-14
3	119	34.0	119	2	US-08-274-215A-12
4	119	34.0	119	2	US-08-765-662-12
5	119	34.0	119	3	US-09-184-933-12
6	119	34.0	119	5	PCT-US95-08745-12
7	15	4.3	106	1	US-08-482-577B-24
8	15	4.3	106	3	US-08-289-222E-28
9	15	4.3	106	3	US-09-218-176-7
10	15	4.3	106	3	US-09-054-526B-28
11	15	4.3	352	1	US-08-482-577B-2
12	15	4.3	352	3	US-08-289-222E-4
13	15	4.3	352	3	US-09-218-176-2
14	15	4.3	352	3	US-09-054-526B-4
15	15	4.3	352	4	US-08-981-490B-3
16	12	3.4	35	4	US-09-374-958C-23
17	11	3.1	352	1	US-08-482-577B-4
18	11	3.1	352	3	US-09-218-176-4
19	11	3.1	352	4	US-08-981-490B-4
20	9	2.6	13	4	US-09-374-958C-74
21	9	2.6	35	4	US-09-374-958C-17
22	9	2.6	35	4	US-09-374-958C-34
23	9	2.6	102	4	US-09-374-958C-87
24	9	2.6	102	4	US-09-374-958C-88
25	9	2.6	117	4	US-09-374-958C-69
26	9	2.6	119	2	US-08-581-528A-7
27	9	2.6	119	4	US-09-412-791D-7

28	9	2.6	119	5	PCT-US94-07799-7	Sequence 7, Appl
29	9	2.6	129	1	US-08-360-914B-15	Sequence 15, Appl
30	9	2.6	129	1	US-08-741-589A-13	Sequence 13, Appl
31	9	2.6	139	4	US-09-374-958C-68	Sequence 68, Appl
32	9	2.6	140	4	US-09-374-958C-90	Sequence 90, Appl
33	9	2.6	160	4	US-09-252-991A-17039	Sequence 17039, A
34	9	2.6	161	2	US-08-581-528A-6	Sequence 6, Appl
35	9	2.6	161	4	US-09-412-791D-6	Sequence 6, Appl
36	9	2.6	161	5	PCT-US94-07799-6	Sequence 6, Appl
37	9	2.6	240	1	US-08-362-670B-30	Sequence 30, Appl
38	9	2.6	240	3	US-08-333-576C-30	Sequence 30, Appl
39	9	2.6	240	3	US-08-808-324-30	Sequence 30, Appl
40	9	2.6	240	3	US-09-945-182-30	Sequence 30, Appl
41	9	2.6	240	5	PCT-US94-14030A-30	Sequence 30, Appl
42	9	2.6	294	1	US-08-362-670B-2	Sequence 2, Appl
43	9	2.6	294	3	US-08-333-576C-2	Sequence 2, Appl
44	9	2.6	294	3	US-08-808-324-2	Sequence 2, Appl
45	9	2.6	294	4	US-09-945-182-2	Sequence 2, Appl
46	9	2.6	294	5	PCT-US94-14030A-2	Sequence 2, Appl
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48	9	2.6	388	3	US-08-333-576C-34	Sequence 34, Appl
49	9	2.6	388	4	US-08-808-324-34	Sequence 34, Appl
50	9	2.6	388	4	US-09-945-182-34	Sequence 34, Appl
51	9	2.6	388	5	PCT-US94-14030A-34	Sequence 34, Appl
52	9	2.6	411	1	US-08-362-670B-28	Sequence 28, Appl
53	9	2.6	411	3	US-08-333-576C-28	Sequence 28, Appl
54	9	2.6	411	3	US-08-808-324-28	Sequence 28, Appl
55	9	2.6	411	4	US-09-945-182-28	Sequence 28, Appl
56	9	2.6	411	5	PCT-US94-14030A-28	Sequence 28, Appl
57	9	2.6	448	4	US-09-902-540-16109	Sequence 16109, A
58	8	2.3	26	3	US-09-218-176-43	Sequence 43, Appl
59	8	2.3	102	4	US-09-252-991A-22067	Sequence 22067, A
60	8	2.3	133	4	US-09-270-767-35839	Sequence 35839, A
61	8	2.3	133	4	US-09-270-767-51056	Sequence 51056, A
62	8	2.3	174	4	US-09-252-991A-26997	Sequence 26997, A
63	8	2.3	185	4	US-09-252-991A-23179	Sequence 23179, A
64	8	2.3	263	4	US-09-252-991A-25669	Sequence 25669, A
65	8	2.3	305	4	US-09-489-039A-9736	Sequence 9736, Ap
66	8	2.3	766	4	US-09-489-039A-12983	Sequence 12983, A
67	8	2.3	792	4	US-09-252-991A-25776	Sequence 25776, A
68	7	2.0	36	4	US-09-287-849-37	Sequence 37, Appl
69	7	2.0	54	4	US-09-513-999C-6694	Sequence 6694, Ap
70	7	2.0	82	4	US-09-248-796A-26301	Sequence 26301, A
71	7	2.0	96	4	US-09-621-976-5451	Sequence 5451, Ap
72	7	2.0	104	4	US-09-270-767-32777	Sequence 32777, A
73	7	2.0	104	4	US-09-270-767-47994	Sequence 47994, A
74	7	2.0	109	4	US-09-489-039A-11675	Sequence 11675, A
75	7	2.0	112	4	US-09-270-767-34076	Sequence 34076, A
76	7	2.0	112	4	US-09-270-767-49293	Sequence 49293, A
77	7	2.0	113	3	US-09-199-637A-307	Sequence 307, App
78	7	2.0	115	1	US-08-152-922A-7	Sequence 7, Appl
79	7	2.0	120	4	US-09-489-039A-12045	Sequence 12045, A
80	7	2.0	126	1	US-08-247-907A-2	Sequence 2, Appl
81	7	2.0	126	1	US-08-452-772-2	Sequence 2, Appl
82	7	2.0	126	2	US-08-765-875-4	Sequence 4, Appl
83	7	2.0	126	3	US-08-795-671-4	Sequence 4, Appl
84	7	2.0	126	3	US-09-414-234-2	Sequence 2, Appl
85	7	2.0	126	4	US-08-919-850-2	Sequence 2, Appl
86	7	2.0	126	4	US-09-454-540-4	Sequence 4, Appl
87	7	2.0	126	5	PCT-US94-05288-2	Sequence 2, Appl
88	7	2.0	127	1	US-08-455-550-11	Sequence 11, Appl
89	7	2.0	135	4	US-10-101-464A-618	Sequence 618, App
90	7	2.0	144	4	US-09-252-991A-16650	Sequence 16650, A
91	7	2.0	145	4	US-09-252-991A-28008	Sequence 28008, A
92	7	2.0	154	4	US-09-248-796A-27732	Sequence 27732, A
93	7	2.0	165	4	US-09-252-991A-19409	Sequence 19409, A
94	7	2.0	166	4	US-09-252-991A-21079	Sequence 21079, A
95	7	2.0	181	4	US-09-252-991A-18426	Sequence 18426, A
96	7	2.0	200	4	US-09-252-991A-24765	Sequence 24765, A
97	7	2.0	217	4	US-09-252-991A-19862	Sequence 19862, A
98	7	2.0	228	3	US-09-724-864-42	Sequence 42, Appl
99	7	2.0	241	4	US-09-902-540-13382	Sequence 13382, A
100	7	2.0	242	4	US-09-252-991A-24652	Sequence 24652, A

101	7	2.0	243	4	US-09-252-991A-19011	Sequence 19011, A	174	7	2.0	693	4	US-09-107-532A-5812	Sequence 5812, Ap
102	7	2.0	250	4	US-09-902-540-13919	Sequence 13919, A	175	7	2.0	720	4	US-09-252-991A-21881	Sequence 21881, A
103	7	2.0	253	4	US-09-252-991A-32459	Sequence 32459, A	176	7	2.0	784	4	US-09-583-110-5192	Sequence 5192, Ap
104	7	2.0	254	4	US-09-252-991A-26135	Sequence 26135, A	177	7	2.0	787	4	US-09-107-433-4612	Sequence 4612, Ap
105	7	2.0	264	4	US-09-252-991A-22289	Sequence 22289, A	178	7	2.0	860	4	US-09-252-991A-25681	Sequence 25681, A
106	7	2.0	275	4	US-09-949-016-11338	Sequence 11338, A	179	7	2.0	920	4	US-09-252-991A-28918	Sequence 28918, A
107	7	2.0	278	4	US-09-252-991A-24928	Sequence 24928, A	180	7	2.0	974	4	US-10-101-464A-921	Sequence 921, App
108	7	2.0	283	4	US-09-252-991A-28431	Sequence 28431, A	181	7	2.0	1024	4	US-09-562-737-47	Sequence 921, App
109	7	2.0	282	4	US-09-252-991A-24509	Sequence 24509, A	182	7	2.0	1058	2	US-08-247-904B-14	Sequence 47, Appl
110	7	2.0	296	4	US-09-673-395A-407	Sequence 407, App	183	7	2.0	1058	3	US-08-767-942A-15	Sequence 15, Appl
111	7	2.0	300	4	US-09-252-991A-17479	Sequence 17479, A	184	7	2.0	1058	4	US-09-826-312A-2	Sequence 2, Appli
112	7	2.0	307	4	US-09-252-991A-21588	Sequence 21588, A	185	7	2.0	1058	4	US-09-538-092-985	Sequence 985, App
113	7	2.0	324	4	US-09-252-991A-22506	Sequence 22506, A	186	7	2.0	1059	4	US-09-542-497A-2	Sequence 2, Appli
114	7	2.0	326	4	US-09-252-991A-30194	Sequence 30194, A	187	7	2.0	1225	4	US-09-252-991A-25018	Sequence 25018, A
115	7	2.0	328	4	US-09-252-991A-28618	Sequence 28618, A	188	7	2.0	1225	4	US-09-252-991A-28988	Sequence 28988, A
116	7	2.0	333	4	US-10-101-464A-561	Sequence 561, App	189	7	2.0	1225	4	US-09-902-540-11252	Sequence 11252, A
117	7	2.0	333	4	US-09-949-016-7304	Sequence 7304, Ap	190	7	2.0	1840	4	US-09-453-702B-257	Sequence 257, App
118	7	2.0	334	1	US-08-482-385A-7	Sequence 7, Appli	191	6	1.7	14	4	US-09-462-246-11	Sequence 11, Appl
119	7	2.0	334	4	US-09-949-016-9846	Sequence 9846, Ap	192	6	1.7	16	2	US-08-433-133-15	Sequence 15, Appl
120	7	2.0	349	4	US-09-252-991A-30661	Sequence 30661, A	193	6	1.7	17	1	US-08-433-133-15	Sequence 9, Appli
121	7	2.0	362	1	US-08-247-907A-11	Sequence 11, Appl	194	6	1.7	20	6	5496552-19	Patent No. 5496552
122	7	2.0	362	1	US-08-452-772-11	Sequence 11, Appl	195	6	1.7	20	6	5496552-19	Patent No. 5496552
123	7	2.0	362	3	US-09-414-234-11	Sequence 11, Appl	196	6	1.7	21	1	US-08-786-748A-123	Sequence 123, App
124	7	2.0	362	4	US-08-919-850-11	Sequence 11, Appl	197	6	1.7	21	2	US-08-932-682-123	Sequence 123, App
125	7	2.0	362	5	PCT-US94-05288-11	Sequence 11, Appl	198	6	1.7	25	2	US-08-480-473B-55	Sequence 55, Appl
126	7	2.0	367	4	US-09-252-991A-20708	Sequence 20708, A	199	6	1.7	25	3	US-08-915-213-55	Sequence 55, Appl
127	7	2.0	379	4	US-09-252-991A-31693	Sequence 31693, A	200	6	1.7	25	3	US-08-235-217-55	Sequence 55, Appl
128	7	2.0	395	4	US-09-673-395A-612	Sequence 612, App	201	6	1.7	28	2	US-08-433-133-92	Sequence 92, Appl
129	7	2.0	401	4	US-09-489-039A-12481	Sequence 12481, A	202	6	1.7	28	3	US-09-082-279B-50	Sequence 50, Appl
130	7	2.0	401	4	US-09-949-016-8223	Sequence 8223, Ap	203	6	1.7	28	3	US-09-315-304B-50	Sequence 50, Appl
131	7	2.0	407	2	US-08-765-875-2	Sequence 2, Appli	204	6	1.7	28	4	US-09-834-784-50	Sequence 50, Appl
132	7	2.0	407	2	US-08-765-875-6	Sequence 6, Appli	205	6	1.7	28	4	US-09-515-965A-50	Sequence 50, Appl
133	7	2.0	407	3	US-08-795-671-2	Sequence 2, Appli	206	6	1.7	28	4	US-09-350-641C-50	Sequence 50, Appl
134	7	2.0	407	3	US-08-795-671-6	Sequence 6, Appli	207	6	1.7	28	4	US-09-350-641A-50	Sequence 50, Appl
135	7	2.0	407	4	US-09-454-540-2	Sequence 2, Appli	208	6	1.7	33	1	US-08-158-189-25	Sequence 25, Appl
136	7	2.0	407	4	US-09-454-540-6	Sequence 6, Appli	209	6	1.7	33	1	US-08-158-189-26	Sequence 26, Appl
137	7	2.0	407	4	US-09-626-896-25	Sequence 25, Appl	210	6	1.7	33	2	US-08-491-204A-9	Sequence 9, Appli
138	7	2.0	407	4	US-09-485-046-16	Sequence 16, Appl	211	6	1.7	33	2	US-08-491-204A-10	Sequence 10, Appl
139	7	2.0	410	4	US-09-252-991A-32716	Sequence 32716, A	212	6	1.7	33	4	US-09-030-619-185	Sequence 185, App
140	7	2.0	418	4	US-09-252-991A-17463	Sequence 17463, A	213	6	1.7	33	4	US-09-030-619-186	Sequence 186, App
141	7	2.0	419	4	US-09-949-016-7295	Sequence 7295, Ap	214	6	1.7	33	4	US-09-030-619-191	Sequence 191, App
142	7	2.0	425	4	US-09-252-991A-20467	Sequence 20467, A	215	6	1.7	33	4	US-09-030-619-192	Sequence 192, App
143	7	2.0	432	4	US-09-252-991A-22739	Sequence 22739, A	216	6	1.7	33	4	US-09-917-340-42	Sequence 42, Appl
144	7	2.0	432	4	US-09-902-540-15774	Sequence 15774, A	217	6	1.7	33	4	US-09-917-340-43	Sequence 43, Appl
145	7	2.0	436	4	US-09-902-540-9717	Sequence 9717, Ap	218	6	1.7	36	3	US-09-082-279B-1210	Sequence 1210, Ap
146	7	2.0	442	4	US-09-198-452A-903	Sequence 903, App	219	6	1.7	36	3	US-09-315-304B-1210	Sequence 1210, Ap
147	7	2.0	447	4	US-09-902-540-14598	Sequence 14598, A	220	6	1.7	36	4	US-09-834-784-1210	Sequence 1210, Ap
148	7	2.0	462	3	US-08-630-915A-38	Sequence 38, Appl	221	6	1.7	36	4	US-09-515-965A-1210	Sequence 1210, Ap
149	7	2.0	462	4	US-09-879-957-38	Sequence 38, Appl	222	6	1.7	36	4	US-09-350-641C-1210	Sequence 1210, Ap
150	7	2.0	467	4	US-09-492-709A-381	Sequence 381, Appl	223	6	1.7	36	4	US-09-350-641A-1210	Sequence 1210, Ap
151	7	2.0	472	4	US-09-438-185A-840	Sequence 840, App	224	6	1.7	38	3	US-09-082-279B-1180	Sequence 1180, Ap
152	7	2.0	476	4	US-09-252-991A-17561	Sequence 17561, A	225	6	1.7	38	3	US-09-082-279B-1181	Sequence 1181, Ap
153	7	2.0	483	4	US-09-252-991A-27152	Sequence 27152, A	226	6	1.7	38	3	US-09-082-279B-1182	Sequence 1182, Ap
154	7	2.0	483	4	US-09-252-991A-29267	Sequence 29267, A	227	6	1.7	38	3	US-09-082-279B-1183	Sequence 1183, Ap
155	7	2.0	495	4	US-09-252-991A-24607	Sequence 24607, A	228	6	1.7	38	3	US-09-315-304B-1180	Sequence 1180, Ap
156	7	2.0	508	4	US-09-252-991A-32269	Sequence 32269, A	229	6	1.7	38	3	US-09-315-304B-1181	Sequence 1181, Ap
157	7	2.0	520	4	US-09-538-092-1347	Sequence 1347, Ap	230	6	1.7	38	3	US-09-315-304B-1182	Sequence 1182, Ap
158	7	2.0	525	4	US-09-252-991A-31946	Sequence 31946, A	231	6	1.7	38	3	US-09-315-304B-1183	Sequence 1183, Ap
159	7	2.0	530	4	US-09-252-991A-23861	Sequence 23861, A	232	6	1.7	38	4	US-09-834-784-1181	Sequence 1181, Ap
160	7	2.0	547	1	US-08-340-203A-3	Sequence 3, Appli	233	6	1.7	38	4	US-09-834-784-1181	Sequence 1181, Ap
161	7	2.0	547	2	US-08-452-567-3	Sequence 3, Appli	234	6	1.7	38	4	US-09-834-784-1182	Sequence 1182, Ap
162	7	2.0	547	2	US-08-452-427-3	Sequence 3, Appli	235	6	1.7	38	4	US-09-834-784-1183	Sequence 1183, Ap
163	7	2.0	547	3	US-09-085-407-3	Sequence 3, Appli	236	6	1.7	38	4	US-09-515-965A-1180	Sequence 1180, Ap
164	7	2.0	557	4	US-09-252-991A-28083	Sequence 28083, A	237	6	1.7	38	4	US-09-515-965A-1181	Sequence 1181, Ap
165	7	2.0	561	4	US-09-252-991A-26778	Sequence 26778, A	238	6	1.7	38	4	US-09-515-965A-1182	Sequence 1182, Ap
166	7	2.0	579	4	US-09-252-991A-32124	Sequence 32124, A	239	6	1.7	38	4	US-09-515-965A-1183	Sequence 1183, Ap
167	7	2.0	603	4	US-09-252-991A-25038	Sequence 25038, A	240	6	1.7	38	4	US-09-350-641C-1180	Sequence 1180, Ap
168	7	2.0	605	4	US-09-252-991A-18837	Sequence 18837, A	241	6	1.7	38	4	US-09-350-641C-1181	Sequence 1181, Ap
169	7	2.0	620	4	US-09-934-903-2	Sequence 2, Appli	242	6	1.7	38	4	US-09-350-641C-1182	Sequence 1182, Ap
170	7	2.0	620	4	US-09-934-868-62	Sequence 62, Appl	243	6	1.7	38	4	US-09-350-641C-1183	Sequence 1183, Ap
171	7	2.0	655	3	US-09-252-991A-17112	Sequence 17112, A	244	6	1.7	38	4	US-09-270-767-35903	Sequence 35903, A
172	7	2.0	690	3	US-09-1228-986-69	Sequence 69, Appl	245	6	1.7	38	4	US-09-270-767-51120	Sequence 51120, A
173	7	2.0	690	4	US-10-101-464A-69	Sequence 69, Appl	246	6	1.7	38	4	US-09-350-641A-1180	Sequence 1180, Ap

247	6	1.7	38	4	US-09-350-841A-1181	Sequence 1181, Ap	320	6	1.7	77	4	US-09-723-890-21	Sequence 21, Appl
248	6	1.7	38	4	US-09-350-841A-1182	Sequence 1182, Ap	321	6	1.7	77	4	US-09-723-901-21	Sequence 21, Appl
249	6	1.7	38	4	US-09-350-841A-1183	Sequence 1183, Ap	322	6	1.7	77	4	US-09-723-547-21	Sequence 21, Appl
250	6	1.7	39	4	US-08-733-622C-35	Sequence 35, Appl	323	6	1.7	77	4	US-09-724-127-21	Sequence 21, Appl
251	6	1.7	40	3	US-09-082-279B-1211	Sequence 1211, Ap	324	6	1.7	77	4	US-09-723-931-21	Sequence 21, Appl
252	6	1.7	40	3	US-09-315-304B-1211	Sequence 1211, Ap	325	6	1.7	77	4	US-09-723-873-21	Sequence 21, Appl
253	6	1.7	40	4	US-09-834-784-1211	Sequence 1211, Ap	326	6	1.7	77	4	US-09-724-114-21	Sequence 21, Appl
254	6	1.7	40	4	US-09-515-965A-1211	Sequence 1211, Ap	327	6	1.7	77	4	US-09-723-913-21	Sequence 21, Appl
255	6	1.7	40	4	US-09-350-641C-1211	Sequence 1211, Ap	328	6	1.7	77	4	US-09-723-912-21	Sequence 21, Appl
256	6	1.7	40	4	US-09-350-841A-1211	Sequence 1211, Ap	329	6	1.7	77	4	US-09-724-095-21	Sequence 21, Appl
257	6	1.7	45	4	US-09-612-402B-33	Sequence 33, Appl	330	6	1.7	77	4	US-09-724-157-21	Sequence 21, Appl
258	6	1.7	46	2	US-08-480-473B-54	Sequence 54, Appl	331	6	1.7	77	4	US-09-270-767-57875	Sequence 57875, A
259	6	1.7	46	3	US-08-915-213-54	Sequence 54, Appl	332	6	1.7	77	4	US-09-724-062-21	Sequence 21, Appl
260	6	1.7	46	3	US-09-235-217-54	Sequence 54, Appl	333	6	1.7	77	4	US-09-724-065-21	Sequence 21, Appl
261	6	1.7	46	3	US-09-227-357-540	Sequence 540, App	334	6	1.7	78	4	US-09-489-039A-8935	Sequence 8935, Ap
262	6	1.7	50	2	US-08-766-858A-39	Sequence 39, Appl	335	6	1.7	80	4	US-09-270-767-39725	Sequence 39725, A
263	6	1.7	53	4	US-09-471-276-1393	Sequence 1393, Ap	336	6	1.7	80	4	US-09-270-767-54942	Sequence 54942, A
264	6	1.7	58	4	US-09-621-976-1393	Sequence 1393, Ap	337	6	1.7	82	4	US-09-248-796A-24266	Sequence 24266, A
265	6	1.7	60	2	US-08-637-759B-381	Sequence 7048, Ap	338	6	1.7	83	4	US-09-248-796A-26013	Sequence 26013, A
266	6	1.7	60	3	US-08-871-355A-381	Sequence 381, App	339	6	1.7	83	4	US-09-107-532A-5281	Sequence 5281, Ap
267	6	1.7	60	3	US-09-201-945-381	Sequence 381, App	340	6	1.7	84	4	US-09-902-540-12932	Sequence 12932, A
268	6	1.7	60	4	US-09-248-796A-24221	Sequence 24221, A	341	6	1.7	88	3	US-08-513-974B-338	Sequence 338, App
269	6	1.7	61	4	US-09-513-999C-7338	Sequence 7338, Ap	342	6	1.7	88	3	US-08-513-974B-339	Sequence 339, App
270	6	1.7	63	4	US-09-621-976-4553	Sequence 4553, Ap	343	6	1.7	89	4	US-09-270-767-60514	Sequence 60514, A
271	6	1.7	64	4	US-09-107-532A-6960	Sequence 6960, Ap	344	6	1.7	91	4	US-09-690-454-75	Sequence 75, Appl
272	6	1.7	64	4	US-09-612-402B-34	Sequence 34, Appl	345	6	1.7	92	1	US-07-807-529A-2	Sequence 2, Appl1
273	6	1.7	64	4	US-09-248-796A-26631	Sequence 26631, A	346	6	1.7	92	5	PCT-US93-02462-2	Sequence 2, Appl1
274	6	1.7	64	4	US-09-248-796A-27359	Sequence 27359, A	347	6	1.7	94	3	US-07-662-193-1	Sequence 1, Appl1
275	6	1.7	65	4	US-09-107-532A-5412	Sequence 5412, Ap	348	6	1.7	94	3	US-08-300-928C-2	Sequence 2, Appl1
276	6	1.7	65	4	US-09-248-796A-27283	Sequence 27283, A	349	6	1.7	94	3	US-08-300-928C-11	Sequence 11, Appl
277	6	1.7	65	4	US-09-248-796A-27863	Sequence 27863, A	350	6	1.7	94	3	US-08-430-944D-2	Sequence 2, Appl1
278	6	1.7	65	4	5320958-17	Patent No. 5320958	351	6	1.7	94	3	US-08-430-944D-11	Sequence 11, Appl
279	6	1.7	65	6	5320958-17	Patent No. 5320958	352	6	1.7	94	3	US-08-430-014-2	Sequence 2, Appl1
280	6	1.7	68	4	US-09-621-976-6572	Sequence 6572, Ap	353	6	1.7	94	3	US-08-430-014-11	Sequence 11, Appl
281	6	1.7	70	4	US-09-270-767-33571	Sequence 33571, A	354	6	1.7	94	3	US-08-431-184-2	Sequence 2, Appl1
282	6	1.7	70	4	US-09-270-767-48788	Sequence 48788, A	355	6	1.7	94	3	US-08-431-184-11	Sequence 11, Appl
283	6	1.7	70	4	US-09-248-796A-27390	Sequence 27390, A	356	6	1.7	95	1	US-08-158-189-14	Sequence 14, Appl
284	6	1.7	71	3	US-08-513-974B-44	Sequence 44, Appl	357	6	1.7	95	1	US-08-158-189-15	Sequence 15, Appl
285	6	1.7	71	4	US-09-461-436B-44	Sequence 44, Appl	358	6	1.7	95	1	US-08-519-777-23	Sequence 23, Appl
286	6	1.7	72	1	US-08-362-670B-13	Sequence 13, Appl	359	6	1.7	95	1	US-08-519-777-24	Sequence 24, Appl
287	6	1.7	72	3	US-08-333-576C-13	Sequence 13, Appl	360	6	1.7	95	1	US-08-742-035-23	Sequence 23, Appl
288	6	1.7	72	3	US-08-808-324-13	Sequence 36241, A	361	6	1.7	95	1	US-08-742-035-24	Sequence 24, Appl
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290	6	1.7	72	4	US-09-270-767-51458	Sequence 51458, A	363	6	1.7	95	2	US-08-777-019-24	Sequence 24, Appl
291	6	1.7	72	4	US-09-945-182-13	Sequence 13, Appl	364	6	1.7	95	2	US-08-777-143-23	Sequence 23, Appl
292	6	1.7	72	5	PCT-US94-14030A-13	Sequence 13, Appl	365	6	1.7	95	2	US-08-777-143-24	Sequence 24, Appl
293	6	1.7	75	4	US-09-621-976-4264	Sequence 4264, Ap	366	6	1.7	95	3	US-08-775-414-23	Sequence 23, Appl
294	6	1.7	76	1	US-08-519-777-19	Sequence 19, Appl	367	6	1.7	95	3	US-08-775-414-24	Sequence 24, Appl
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296	6	1.7	76	1	US-08-742-035-19	Sequence 19, Appl	369	6	1.7	95	3	US-08-931-858E-24	Sequence 24, Appl
297	6	1.7	76	1	US-08-742-035-22	Sequence 22, Appl	370	6	1.7	95	3	US-08-981-739-23	Sequence 23, Appl
298	6	1.7	76	2	US-08-777-019-19	Sequence 19, Appl	371	6	1.7	95	3	US-08-981-739-24	Sequence 24, Appl
299	6	1.7	76	2	US-08-777-019-22	Sequence 22, Appl	372	6	1.7	95	4	US-09-128-026-23	Sequence 23, Appl
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301	6	1.7	76	2	US-08-777-143-22	Sequence 22, Appl	374	6	1.7	95	4	US-09-220-616-23	Sequence 23, Appl
302	6	1.7	76	3	US-08-775-414-19	Sequence 19, Appl	375	6	1.7	95	4	US-09-220-616-24	Sequence 24, Appl
303	6	1.7	76	3	US-08-775-414-22	Sequence 22, Appl	376	6	1.7	95	4	US-09-220-527-23	Sequence 23, Appl
304	6	1.7	76	3	US-08-931-858E-19	Sequence 19, Appl	377	6	1.7	95	4	US-09-220-527-24	Sequence 24, Appl
305	6	1.7	76	3	US-08-931-858E-22	Sequence 22, Appl	378	6	1.7	95	4	US-09-917-340-76	Sequence 76, Appl
306	6	1.7	76	3	US-08-981-739-19	Sequence 19, Appl	379	6	1.7	95	4	US-09-220-407-23	Sequence 23, Appl
307	6	1.7	76	3	US-08-981-739-22	Sequence 22, Appl	380	6	1.7	95	4	US-09-220-407-24	Sequence 24, Appl
308	6	1.7	76	4	US-09-128-026-19	Sequence 19, Appl	381	6	1.7	95	4	US-09-219-952-23	Sequence 23, Appl
309	6	1.7	76	4	US-09-128-026-22	Sequence 22, Appl	382	6	1.7	95	4	US-09-219-952-24	Sequence 24, Appl
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312	6	1.7	76	4	US-09-220-527-19	Sequence 19, Appl	385	6	1.7	98	4	US-09-513-999C-6080	Sequence 6080, Ap
313	6	1.7	76	4	US-09-220-527-22	Sequence 22, Appl	386	6	1.7	99	3	US-08-931-858E-170	Sequence 170, App
314	6	1.7	76	4	US-09-220-407-19	Sequence 19, Appl	387	6	1.7	99	3	US-08-981-739-170	Sequence 170, App
315	6	1.7	76	4	US-09-220-407-22	Sequence 22, Appl	388	6	1.7	99	4	US-09-128-026-170	Sequence 170, App
316	6	1.7	76	4	US-09-219-952-19	Sequence 19, Appl	389	6	1.7	99	4	US-09-220-616-170	Sequence 170, App
317	6	1.7	76	4	US-09-219-952-22	Sequence 22, Appl	390	6	1.7	99	4	US-09-220-527-170	Sequence 170, App
318	6	1.7	77	3	US-08-825-852-21	Sequence 21, Appl	391	6	1.7	99	4	US-09-220-407-170	Sequence 170, App
319	6	1.7	77	3	US-09-052-888-21	Sequence 21, Appl	392	6	1.7	102	4	US-09-374-958C-84	Sequence 84, Appl

393	6	1.7	102	4	US-09-374-958C-85	Sequence 85, Appl
394	6	1.7	102	4	US-09-374-958C-86	Sequence 86, Appl
395	6	1.7	103	4	US-09-513-999C-5877	Sequence 5877, Ap
396	6	1.7	105	1	US-08-482-577B-27	Sequence 27, Appl
397	6	1.7	105	3	US-08-478-097A-22	Sequence 22, Appl
398	6	1.7	105	3	US-08-289-222E-31	Sequence 31, Appl
399	6	1.7	105	3	US-09-218-176-10	Sequence 10, Appl
400	6	1.7	105	3	US-09-054-526B-31	Sequence 31, Appl
401	6	1.7	105	3	US-08-931-858E-169	Sequence 169, App
402	6	1.7	105	3	US-09-001-472-2	Sequence 2, Appl1
403	6	1.7	105	3	US-08-981-739-169	Sequence 169, App
404	6	1.7	105	4	US-09-128-026-169	Sequence 169, App
405	6	1.7	105	4	US-09-071-035-292	Sequence 292, App
406	6	1.7	105	4	US-08-857-389-26	Sequence 26, Appl
407	6	1.7	105	4	US-09-496-398-22	Sequence 22, Appl
408	6	1.7	105	4	US-09-775-827A-2	Sequence 2, Appl1
409	6	1.7	105	4	US-09-775-827A-13	Sequence 13, Appl
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412	6	1.7	105	4	US-09-732-210-1291	Sequence 1291, Ap
413	6	1.7	105	4	US-09-220-616-169	Sequence 169, App
414	6	1.7	105	4	US-09-374-958C-61	Sequence 61, Appl
415	6	1.7	105	4	US-09-220-527-169	Sequence 169, App
416	6	1.7	105	4	US-09-220-407-169	Sequence 169, App
417	6	1.7	105	4	US-09-766-396-26	Sequence 26, Appl
418	6	1.7	106	1	US-08-482-577B-25	Sequence 25, Appl
419	6	1.7	106	3	US-08-478-097A-23	Sequence 23, Appl
420	6	1.7	106	3	US-08-289-222E-29	Sequence 29, Appl
421	6	1.7	106	3	US-09-218-176-8	Sequence 8, Appl1
422	6	1.7	106	3	US-09-054-526B-29	Sequence 29, Appl
423	6	1.7	106	3	US-08-931-858E-153	Sequence 153, App
424	6	1.7	106	3	US-08-981-739-153	Sequence 153, App
425	6	1.7	106	4	US-09-128-026-153	Sequence 153, App
426	6	1.7	106	4	US-09-378-238-36	Sequence 36, Appl
427	6	1.7	106	4	US-09-496-398-23	Sequence 23, Appl
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432	6	1.7	106	4	US-09-374-958C-63	Sequence 63, Appl
433	6	1.7	106	4	US-09-220-527-153	Sequence 153, App
434	6	1.7	106	4	US-09-220-407-153	Sequence 153, App
435	6	1.7	107	4	US-09-252-991A-32005	Sequence 32005, A
436	6	1.7	107	4	US-09-489-039A-7336	Sequence 7336, Ap
437	6	1.7	108	4	US-09-252-991A-29540	Sequence 29540, A
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439	6	1.7	109	1	US-08-271-252-4	Sequence 4, Appl1
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441	6	1.7	111	4	US-09-513-999C-8147	Sequence 8147, Ap
442	6	1.7	114	4	US-09-513-999C-6218	Sequence 6218, Ap
443	6	1.7	115	1	US-08-481-377-19	Sequence 19, Appl
444	6	1.7	115	2	US-08-491-835-17	Sequence 17, Appl
445	6	1.7	115	3	US-09-153-733A-19	Sequence 19, Appl
446	6	1.7	115	3	US-08-946-092A-17	Sequence 17, Appl
447	6	1.7	115	3	US-09-172-062-17	Sequence 17, Appl
448	6	1.7	115	3	US-09-301-520D-17	Sequence 17, Appl
449	6	1.7	115	3	US-09-389-705-19	Sequence 19, Appl
450	6	1.7	115	5	PCT-US94-00666-19	Sequence 19, Appl
451	6	1.7	115	5	PCT-US94-00685-17	Sequence 17, Appl
452	6	1.7	116	1	US-08-197-792-35	Sequence 35, Appl
453	6	1.7	116	1	US-08-197-792-38	Sequence 38, Appl
454	6	1.7	116	1	US-08-459-850-35	Sequence 35, Appl
455	6	1.7	116	1	US-08-459-850-38	Sequence 38, Appl
456	6	1.7	116	1	US-08-459-214-35	Sequence 35, Appl
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460	6	1.7	116	2	US-08-525-596B-25	Sequence 25, Appl
461	6	1.7	116	2	US-08-581-528A-15	Sequence 15, Appl
462	6	1.7	116	3	US-09-097-616-15	Sequence 15, Appl
463	6	1.7	116	3	US-09-177-860A-25	Sequence 25, Appl
464	6	1.7	116	3	US-08-624-635-17	Sequence 17, Appl
465	6	1.7	116	3	US-09-145-060-21	Sequence 21, Appl
466	6	1.7	116	4	US-09-378-238-35	Sequence 35, Appl
467	6	1.7	116	4	US-09-629-938-25	Sequence 25, Appl
468	6	1.7	116	4	US-09-686-344-43	Sequence 43, Appl
469	6	1.7	116	4	US-09-412-791D-15	Sequence 15, Appl
470	6	1.7	116	4	US-09-619-061-15	Sequence 15, Appl
471	6	1.7	116	5	PCT-US94-00657-21	Sequence 21, Appl
472	6	1.7	116	5	PCT-US94-07762-15	Sequence 15, Appl
473	6	1.7	116	5	PCT-US94-07799-15	Sequence 15, Appl
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478	6	1.7	117	3	US-09-175-229-6	Sequence 6, Appl1
479	6	1.7	117	5	PCT-US95-06764-6	Sequence 6, Appl1
480	6	1.7	118	3	US-09-199-637A-279	Sequence 279, App
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484	6	1.7	119	2	US-08-460-402-11	Sequence 11, Appl
485	6	1.7	119	3	US-09-097-616-7	Sequence 7, Appl1
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487	6	1.7	119	4	US-09-619-061-7	Sequence 7, Appl1
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494	6	1.7	121	2	US-08-491-835-19	Sequence 19, Appl
495	6	1.7	121	2	US-09-153-733A-20	Sequence 20, Appl
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497	6	1.7	121	3	US-08-946-092A-18	Sequence 18, Appl
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499	6	1.7	121	3	US-09-172-062-18	Sequence 18, Appl
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507	6	1.7	121	4	US-09-621-976-6925	Sequence 6925, Ap
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510	6	1.7	121	5	PCT-US94-00685-18	Sequence 18, Appl
511	6	1.7	121	5	PCT-US94-00685-19	Sequence 19, Appl
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518	6	1.7	122	2	US-08-525-596B-27	Sequence 27, Appl
519	6	1.7	122	2	US-08-581-528A-16	Sequence 16, Appl
520	6	1.7	122	2	US-08-581-528A-17	Sequence 17, Appl
521	6	1.7	122	3	US-09-097-616-16	Sequence 16, Appl
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525	6	1.7	122	4	US-09-629-938-26	Sequence 26, Appl
526	6	1.7	122	4	US-09-629-938-27	Sequence 27, Appl
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528	6	1.7	122	4	US-09-686-344-45	Sequence 45, Appl
529	6	1.7	122	4	US-09-412-791D-16	Sequence 16, Appl
530	6	1.7	122	4	US-09-412-791D-17	Sequence 17, Appl
531	6	1.7	122	4	US-09-619-061-16	Sequence 16, Appl
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533	6	1.7	122	4	US-09-619-061-18	Sequence 18, Appl
534	6	1.7	122	4	US-09-619-061-19	Sequence 19, Appl
535	6	1.7	122	4	US-09-619-061-20	Sequence 20, Appl
536	6	1.7	122	4	US-09-619-061-21	Sequence 21, Appl
537	6	1.7	122	4	US-09-619-061-22	Sequence 22, Appl
538	6	1.7	122	4	US-09-619-061-23	Sequence 23, Appl

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540	6	1.7	122	5	PCT-US94-00657-23	Sequence 23, Appl	613	6	1.7	140	4	US-09-252-991A-23924	Sequence 23924, A
541	6	1.7	122	5	PCT-US94-07762-16	Sequence 16, Appl	614	6	1.7	140	4	US-09-489-039A-7553	Sequence 7553, Ap
542	6	1.7	122	5	PCT-US94-07762-17	Sequence 17, Appl	615	6	1.7	141	4	US-09-252-991A-19681	Sequence 19681, A
543	6	1.7	122	5	PCT-US94-07799-16	Sequence 16, Appl	616	6	1.7	141	4	US-09-252-991A-20549	Sequence 20549, A
544	6	1.7	122	5	PCT-US94-07799-17	Sequence 17, Appl	617	6	1.7	141	4	US-09-252-991A-25829	Sequence 25829, A
545	6	1.7	123	4	US-09-252-991A-30802	Sequence 30802, A	618	6	1.7	141	4	US-09-583-110-4779	Sequence 4779, Ap
546	6	1.7	124	4	US-09-270-767-32001	Sequence 32001, A	619	6	1.7	142	3	US-08-775-414-82	Sequence 82, Appl
547	6	1.7	124	4	US-09-270-767-47218	Sequence 47218, A	620	6	1.7	142	4	US-09-270-767-40599	Sequence 40599, A
548	6	1.7	127	4	US-09-893-737-48	Sequence 48, Appl	621	6	1.7	142	4	US-09-270-767-55815	Sequence 55815, A
549	6	1.7	129	4	US-09-270-767-37348	Sequence 37348, A	622	6	1.7	142	4	US-09-219-952-82	Sequence 82, Appl
550	6	1.7	129	4	US-09-270-767-52565	Sequence 52565, A	623	6	1.7	143	4	US-09-252-991A-28392	Sequence 28392, A
551	6	1.7	129	4	US-09-949-016-8110	Sequence 8110, Ap	624	6	1.7	143	4	US-09-270-767-37886	Sequence 37886, A
552	6	1.7	130	1	US-08-225-989-21	Sequence 21, Appl	625	6	1.7	143	4	US-09-270-767-53103	Sequence 53103, A
553	6	1.7	130	1	US-08-455-550-9	Sequence 9, Appl	626	6	1.7	144	3	US-08-775-414-81	Sequence 81, Appl
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555	6	1.7	130	3	US-08-580-014-21	Sequence 21, Appl	628	6	1.7	144	4	US-09-219-952-81	Sequence 81, Appl
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561	6	1.7	131	4	US-09-621-976-5133	Sequence 5133, Ap	634	6	1.7	147	4	US-09-540-236-2273	Sequence 2273, Ap
562	6	1.7	131	4	US-10-170-097-654	Sequence 654, App	635	6	1.7	147	4	US-09-489-039A-14211	Sequence 14211, A
563	6	1.7	131	4	US-09-902-540-11259	Sequence 11259, A	636	6	1.7	148	4	US-09-248-796A-16976	Sequence 16976, A
564	6	1.7	132	4	US-09-252-991A-19533	Sequence 19533, A	637	6	1.7	149	4	US-09-107-433-3583	Sequence 3583, Ap
565	6	1.7	132	4	US-09-621-976-4084	Sequence 4084, Ap	638	6	1.7	149	4	US-09-949-016-10945	Sequence 10945, A
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571	6	1.7	134	3	US-09-097-616-6	Sequence 6, Appl	644	6	1.7	152	4	US-09-252-991A-19039	Sequence 19039, A
572	6	1.7	134	4	US-09-570-921-30	Sequence 30, Appl	645	6	1.7	152	4	US-09-219-952-83	Sequence 83, Appl
573	6	1.7	134	4	US-09-570-921-31	Sequence 31, Appl	646	6	1.7	153	4	US-09-252-991A-27025	Sequence 27025, A
574	6	1.7	134	4	US-09-570-921-32	Sequence 32, Appl	647	6	1.7	154	4	US-09-248-796A-14119	Sequence 14119, A
575	6	1.7	134	4	US-09-570-921-33	Sequence 33, Appl	648	6	1.7	154	4	US-09-248-796A-14322	Sequence 14322, A
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577	6	1.7	134	4	US-09-570-921-35	Sequence 35, Appl	650	6	1.7	156	4	US-09-252-991A-32450	Sequence 32450, A
578	6	1.7	134	4	US-09-570-921-37	Sequence 37, Appl	651	6	1.7	156	4	US-09-248-796A-24761	Sequence 24761, A
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587	6	1.7	134	4	US-09-326-402C-14	Sequence 14, Appl	660	6	1.7	164	3	US-09-134-001C-5217	Sequence 5217, Ap
588	6	1.7	134	5	PCT-US94-07762-6	Sequence 6, Appl	661	6	1.7	164	3	US-09-249-697A-9	Sequence 9, Appl
589	6	1.7	135	2	US-08-647-960-3	Sequence 3, Appl	662	6	1.7	164	3	US-09-363-316B-9	Sequence 9, Appl
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591	6	1.7	135	3	US-08-050-259B-20	Sequence 20, Appl	664	6	1.7	164	4	US-09-252-991A-28741	Sequence 28741, A
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593	6	1.7	135	3	US-09-489-292-2	Sequence 2, Appl	666	6	1.7	164	4	US-09-981-649A-9	Sequence 9, Appl
594	6	1.7	135	4	US-08-719-579-2	Sequence 2, Appl	667	6	1.7	165	4	US-09-252-991A-17601	Sequence 17601, A
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596	6	1.7	135	4	US-09-252-991A-27592	Sequence 27592, A	669	6	1.7	166	4	US-09-252-991A-27263	Sequence 27263, A
597	6	1.7	135	4	US-09-919-172-91	Sequence 91, Appl	670	6	1.7	166	4	US-09-543-681A-8078	Sequence 8078, Ap
598	6	1.7	135	4	US-09-976-594-628	Sequence 628, App	671	6	1.7	166	4	US-09-134-000C-5521	Sequence 5521, Ap
599	6	1.7	135	4	US-09-540-236-3329	Sequence 3329, App	672	6	1.7	169	4	US-09-252-991A-18888	Sequence 18888, A
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604	6	1.7	136	4	US-09-732-210-1670	Sequence 1670, Ap	677	6	1.7	172	4	US-09-270-767-44743	Sequence 44743, A
605	6	1.7	137	4	US-09-902-540-13403	Sequence 13403, A	678	6	1.7	173	4	US-09-252-991A-17716	Sequence 17716, A
606	6	1.7	138	4	US-09-252-991A-19261	Sequence 19261, A	679	6	1.7	173	4	US-09-252-991A-18184	Sequence 18184, A
607	6	1.7	138	4	US-09-732-210-633	Sequence 633, App	680	6	1.7	173	4	US-09-252-991A-23777	Sequence 23777, A
608	6	1.7	138	4	US-09-732-210-636	Sequence 636, App	681	6	1.7	173	4	US-09-252-991A-23800	Sequence 23800, A
609	6	1.7	138	4	US-09-270-767-32742	Sequence 32742, A	682	6	1.7	173	4	US-09-252-991A-24327	Sequence 24327, A
610	6	1.7	138	4	US-09-270-767-47959	Sequence 47959, A	683	6	1.7	173	4	US-09-252-991A-25580	Sequence 25580, A
611	6	1.7	138	4	US-09-248-796A-16952	Sequence 16952, A	684	6	1.7	174	4	US-09-252-991A-18735	Sequence 18735, A

685	6	1.7	174	4	US-09-252-991A-20205	Sequence 20205, A
686	6	1.7	174	4	US-09-248-796A-19813	Sequence 19813, A
687	6	1.7	174	4	US-09-248-796A-24013	Sequence 24013, A
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689	6	1.7	175	4	US-09-252-991A-32945	Sequence 32945, A
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691	6	1.7	175	4	US-09-270-767-34229	Sequence 34229, A
692	6	1.7	175	4	US-09-270-767-49446	Sequence 49446, A
693	6	1.7	175	5	PCT-US95-13662A-5	Sequence 5, Appl1
694	6	1.7	176	4	US-09-252-991A-20852	Sequence 20852, A
695	6	1.7	176	4	US-09-734-492A-28	Sequence 28, Appl
696	6	1.7	178	4	US-09-270-767-60879	Sequence 60879, A
697	6	1.7	179	4	US-09-252-991A-25298	Sequence 25298, A
698	6	1.7	179	4	US-09-252-991A-26223	Sequence 26223, A
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701	6	1.7	180	4	US-09-252-991A-31056	Sequence 31056, A
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705	6	1.7	181	4	US-10-012-542-196	Sequence 196, App
706	6	1.7	181	4	US-10-115-123-196	Sequence 196, App
707	6	1.7	182	4	US-09-252-991A-22288	Sequence 22288, A
708	6	1.7	182	4	US-09-252-991A-26590	Sequence 26590, A
709	6	1.7	182	4	US-09-252-991A-29493	Sequence 29493, A
710	6	1.7	182	4	US-09-734-492A-12	Sequence 12, Appl
711	6	1.7	182	4	US-09-734-492A-24	Sequence 24, Appl
712	6	1.7	182	4	US-09-270-767-37041	Sequence 37041, A
713	6	1.7	182	4	US-09-270-767-52258	Sequence 52258, A
714	6	1.7	183	4	US-09-615-192A-303	Sequence 303, App
715	6	1.7	184	2	US-08-078-311-4	Sequence 4, Appl1
716	6	1.7	184	2	US-08-460-402-4	Sequence 4, Appl1
717	6	1.7	184	4	US-09-351-150A-39	Sequence 39, Appl
718	6	1.7	184	4	US-09-252-991A-27862	Sequence 27862, A
719	6	1.7	184	4	US-09-734-492A-8	Sequence 8, Appl1
720	6	1.7	185	4	US-09-252-991A-27520	Sequence 27520, A
721	6	1.7	186	4	US-09-252-991A-24073	Sequence 24073, A
722	6	1.7	188	4	US-09-252-991A-23977	Sequence 23977, A
723	6	1.7	188	4	US-09-198-452A-183	Sequence 183, App
724	6	1.7	188	4	US-09-902-540-12348	Sequence 12348, A
725	6	1.7	189	4	US-09-438-185A-165	Sequence 165, App
726	6	1.7	190	4	US-09-248-796A-16727	Sequence 16727, A
727	6	1.7	191	4	US-09-107-532A-4567	Sequence 4567, Ap
728	6	1.7	192	3	US-09-199-637A-9	Sequence 9, Appl
729	6	1.7	192	4	US-09-252-991A-26562	Sequence 26562, A
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804	6	1.7	220	3	US-09-079-785-19	Sequence 19, Appl
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837	6	1.7	238	4	US-09-606-421B-174	Sequence 174, App
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858	6	1.7	239	4	US-09-229-947-35	Sequence 35, Appl1
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878	6	1.7	247	4	US-09-350-841A-1588	Sequence 1588, App
879	6	1.7	248	4	US-09-252-991A-28060	Sequence 28060, A
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883	6	1.7	249	3	US-08-484-223B-102	Sequence 102, App
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894	6	1.7	250	3	US-08-360-107A-112	Sequence 112, App
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939	6	1.7	279	2	US-08-326-286-8	Sequence 8, Appl1
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955	6	1.7	285	4	US-09-543-681A-5097	Sequence 5097, App
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990	6	1.7	307	4	US-09-949-016-9818	Sequence 9818, Ap
991	6	1.7	308	4	US-09-461-325-437	Sequence 437, App
992	6	1.7	308	4	US-10-012-542-437	Sequence 437, App
993	6	1.7	308	4	US-10-115-123-437	Sequence 437, App
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997	6	1.7	309	4	US-09-949-016-6485	Sequence 6485, Ap
998	6	1.7	310	4	US-09-252-991A-26213	Sequence 26213, A
999	6	1.7	310	4	US-09-252-991A-29363	Sequence 29363, A
1000	6	1.7	310	4	US-09-270-767-45376	Sequence 45376, A

ALIGNMENTS

RESULT 1
US-08-765-662-14
Sequence 14, Application US/08765662
Patent No. 5929213

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,662
FILING DATE: 28-APR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-765-662-14
Query Match 100.0%; Score 350; DB 2; length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRPDVQLVLTALVRAQGTGVCPSGSGSKLAPOAERALLVLEAKQQLDGLHLSR	60
Db	1	MRPDVQLVLTALVRAQGTGVCPSGSGSKLAPOAERALLVLEAKQQLDGLHLSR	60
Qy	61	PRTHPPQALTRALRLOPGSVAPNGEVIISFATVTDSTAYSLSLTFHLSPTSRSH	120
Db	61	PRTHPPQALTRALRLOPGSVAPNGEVIISFATVTDSTAYSLSLTFHLSPTSRSH	120
Qy	121	LYHARLMLHVLPTLPGLTCLIRFRWGPFRRRRQGSRTLLAEHHTNLGWHITLTPSSGLRG	180
Db	121	LYHARLMLHVLPTLPGLTCLIRFRWGPFRRRRQGSRTLLAEHHTNLGWHITLTPSSGLRG	180
Qy	181	EKSGVLKQLDCRPLNGSTVTGQPRRLDTAGHQPFLELKIRANEPGAGRARRPTTC	240
Db	181	EKSGVLKQLDCRPLNGSTVTGQPRRLDTAGHQPFLELKIRANEPGAGRARRPTTC	240
Qy	241	EPATPLCCRDHYVDFQELGWRDWILOPEGQVLNYSGGCPHLAGSPGIAASFHSAVES	300
Db	241	EPATPLCCRDHYVDFQELGWRDWILOPEGQVLNYSGGCPHLAGSPGIAASFHSAVES	300
Qy	301	LKANNPWPASTSCVPTARRPLSLYLDHNGNVVKTDPDMVVEACGCS	350
Db	301	LKANNPWPASTSCVPTARRPLSLYLDHNGNVVKTDPDMVVEACGCS	350

RESULT 2

PCT-US95-08745-14
Sequence 14, Application PC/TUS9508745

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal
ORIGINAL SOURCE:
PCT-US95-08745-14

Query Match 100.0%; Score 350; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPDVQLVLMALVRAQGTGSVCPSGGSKLAPQAEALVLELAKQILDGLHLSR 60
DB 1 MRLPDVQLVLMALVRAQGTGSVCPSGGSKLAPQAEALVLELAKQILDGLHLSR 60
QY 61 PRITHPPQALTRALRRLQPGSVAPNGEEVISFATVTDSTSAVSSILTFHLSTPRSHH 120
DB 61 PRITHPPQALTRALRRLQPGSVAPNGEEVISFATVTDSTSAVSSILTFHLSTPRSHH 120
QY 121 LYHARLWLHVLPFLPGLCLRIFRWGPRRRRGSRRTLLAEHHTNLGWHHTLLPSSGLRG 180
DB 121 LYHARLWLHVLPFLPGLCLRIFRWGPRRRRGSRRTLLAEHHTNLGWHHTLLPSSGLRG 180
QY 181 EKSGVLKQLDCRPLEGNSTVTGQPRRLDTAGHQQPFLELKIRANEPGAGRARRPTC 240
DB 181 EKSGVLKQLDCRPLEGNSTVTGQPRRLDTAGHQQPFLELKIRANEPGAGRARRPTC 240
QY 241 EPATPLCCRDHYVDFQELGWRDWILOPEGYQLYNCSGQCPHLAGSPGIAAFHSVAFS 300
DB 241 EPATPLCCRDHYVDFQELGWRDWILOPEGYQLYNCSGQCPHLAGSPGIAAFHSVAFS 300
QY 301 LKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDPDMVVEACGCS 350
DB 301 LKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDPDMVVEACGCS 350

RESULT 3

US-08-274-215A-12
Sequence 12, Application US/08274215A
Patent No. 5831054

GENERAL INFORMATION:

APPLICANT: Lee, Se-Jin
APPLICANT: Esquelea, Aurora F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla

STATE: CA
COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/274,215A
FILING DATE: 13-JUL-1994

CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/040001
TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-68-5099

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-274-215A-12

Query Match 34.0%; Score 119; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,1e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 RARRPTCEPATPLCCRDHYVDFQELGWRDWILOPEGYQLYNCSGQCPHLAGSPGIA 291
DB 1 RARRPTCEPATPLCCRDHYVDFQELGWRDWILOPEGYQLYNCSGQCPHLAGSPGIA 60
QY 292 ASFHSVFSLLKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDPDMVVEACGCS 350
DB 61 ASFHSVFSLLKANNPWPASTSCCVPTARRPLSLYLDHNGNVKTDVDPDMVVEACGCS 119

RESULT 4

US-08-765-662-12
Sequence 12, Application US/08765662
Patent No. 5929213

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla

STATE: CA
COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,662
FILING DATE: 28-APR-1997

CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE: internal

ORIGINAL SOURCE:
US-08-765-662-12

Query Match 34.0%; Score 119; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2,1e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 RARRPTCEPATPLCCRDHYVDFQELGWRDWILOPEGYQLYNCSGQCPHLAGSPGIA 291
DB 1 RARRPTCEPATPLCCRDHYVDFQELGWRDWILOPEGYQLYNCSGQCPHLAGSPGIA 60

Qy	292	ASFHSAVFSLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDPDMVEACGCS	350
Db	61	ASFHSAVFSLKANNPWPASTSCCVPTARRPLSLYLIDHNGNVKTDVDPDMVEACGCS	119

RESULT 5

```

US-09-184-933-12
/ Sequence 12, Application US/09184933
/ Patent No. 6130050
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: Esquelea, Aurora F.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson, P.C.
/ STREET: 4225 Executive Square, Suite 1400
/ CITY: La Jolla
/ STATE: CA
/ COUNTRY: US
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows95
/ SOFTWARE: PastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/184,933
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/274,215
/ FILING DATE: 13-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haile, Ph.D., Lisa A.
/ REGISTRATION NUMBER: 38,347
/ REFERENCE/DOCKET NUMBER: 07265/040001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-678-5070
/ TELEFAX: 619-68-5099
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: Internal
US-09-184-933-12

```

Query Match

Query Match	34.0%	Score 119	DB 3	Length 119
Best Local Similarity	100.0%	Pred. No. 2.1e-108		
Matches 119; Conservative	0	Mismatches 0	Indels 0	Gaps 0

QY	232	RARRPTCTCEPATPLCCRRDHYVDEQLGWRDMILQPEGYOLNYCSGCCPRHLA	SPGIA	291
Db	1	RARRPTCTCEPATPLCCRRDHYVDEQLGWRDMILQPEGYOLNYCSGCCPRHLA	SPGIA	60
QY	292	ASFHSAVFSLKANNPWPASTSCCVPTARRPLSLYLHDHNGNVKTDVPMVVEAC	GC	350
Db	61	ASFHSAVFSLKANNPWPASTSCCVPTARRPLSLYLHDHNGNVKTDVPMVVEAC	GC	119

RESULT 6

PCT-US95-08745-12
Sequence 12, Application PC/TUS9508745
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla

STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
PCT-US95-08745-12

Query Match

Query Match	34.0%	Score 119;	DB 5;	Length 119;
Best Local Similarity	100.0%	Pred. No. 2.1e-108;		
Matches 119;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	232	RARRRPTCEPATPLCCRRDHVYDFQELGWRDWILOPEGYQLNCSGQCPHLAGSPGIA	291
Db	1	RARRRPTCEPATPLCCRRDHVYDFQELGWRDWILOPEGYQLNCSGQCPHLAGSPGIA	60
QY	292	ASFSAVFSLTKANNPEWASTSCCVPTARRPLSLLYLDHNGNVKTDVPMVVEACGCS	350
Db	61	ASFSAVFSLTKANNPEWASTSCCVPTARRPLSLLYLDHNGNVKTDVPMVVEACGCS	119

RESULT 7

US-08-482-577B-24
Sequence 24, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARMELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482, 577B

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-577B-24

Query Match 4.3%; Score 15; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 SCCVPTARRPLSLY 327
Db 69 SCCVPTARRPLSLY 83

RESULT 8

US-08-289-222E-28
Sequence 28, Application US/08289222E
Patent No. 6120760

GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-28

Query Match 4.3%; Score 15; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 SCCVPTARRPLSLY 327
Db 69 SCCVPTARRPLSLY 83

RESULT 9

US-09-218-176-7.
Sequence 7, Application US/09218176
Patent No. 6171584

GENERAL INFORMATION:

APPLICANT: HOTTEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, Rolf
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., G Street lobby,
STREET: Suite 330
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,176
FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 11 243.1
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:

NAME: KITTS, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-218-176-7

Query Match 4.3%; Score 15; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 313 SCCVPTARRPLSLY 327
Db 69 SCCVPTARRPLSLY 83

RESULT 10
US-09-054-526B-28
Sequence 28, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: HITTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23,190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-28

Query Match 4.3%; Score 15; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 313 SCCVPTARRPLSLY 327
Db 69 SCCVPTARRPLSLY 83

RESULT 11
US-08-482-577B-2
Sequence 2, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARCELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,577B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-577B-2

Query Match 4.3%; Score 15; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 313 SCCVPTARRPLSLY 327
Db 315 SCCVPTARRPLSLY 329

RESULT 12
US-08-289-222B-4
Sequence 4, Application US/08289222B

Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; TITLE OF INVENTION: FAMILY
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARMELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; STREET: SUITE 330
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,222E
; FILING DATE: 25-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-9021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-289-222E-4

Query Match 4.3%; Score 15; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 SCCVPTARRPLSLY 327
Db 315 SCCVPTARRPLSLY 329

RESULT 13
US-09-218-176-2
; Sequence 2, Application US/09218176
; Patent No. 6171584
; GENERAL INFORMATION:
; APPLICANT: H TTEN, Gertrud
; APPLICANT: NEIDHARDT, Helge
; APPLICANT: BECHTOLD, Rolf
; APPLICANT: POHL, Jens
; APPLICANT: PAULISTA, Michael

; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
; TITLE OF INVENTION: TGF- FAMILY
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARMELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., G Street Lobby,
; STREET: Suite 330
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/218,176
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03065
; FILING DATE: 12-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 2-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,577
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92 102 324.8
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 11 243.1
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-6010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-218-176-2

Query Match 4.3%; Score 15; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 SCCVPTARRPLSLY 327
Db 315 SCCVPTARRPLSLY 329

RESULT 14
US-09-054-526B-4
; Sequence 4, Application US/09054526B
; Patent No. 6197550
; GENERAL INFORMATION:
; APPLICANT: H TTEN, GERTRUD

APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARIELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,5268
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-4

Query Match 4.3%; Score 15; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. NO. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 SCCVPTARRPLSLY 327
Db 315 SCCVPTARRPLSLY 329

RESULT 15
US-08-981-490B-3
Sequence 3, Application US/08981490B
Patent No. 6531450
GENERAL INFORMATION:
APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Bechtold, Rolf
APPLICANT: Paulsca, Michael
APPLICANT: Unsicker, Klaus
TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
FILE REFERENCE: 100564-07032
CURRENT APPLICATION NUMBER: US/08/981,490B

CURRENT FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: DE/195 25 416.3
PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-08-981-490B-3

Query Match 4.3%; Score 15; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. NO. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 SCCVPTARRPLSLY 327
Db 315 SCCVPTARRPLSLY 329

Search completed: October 13, 2005, 18:47:48
Job time : 62 secs